Figure 1

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Filed: 05 March 2004

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Figure 2

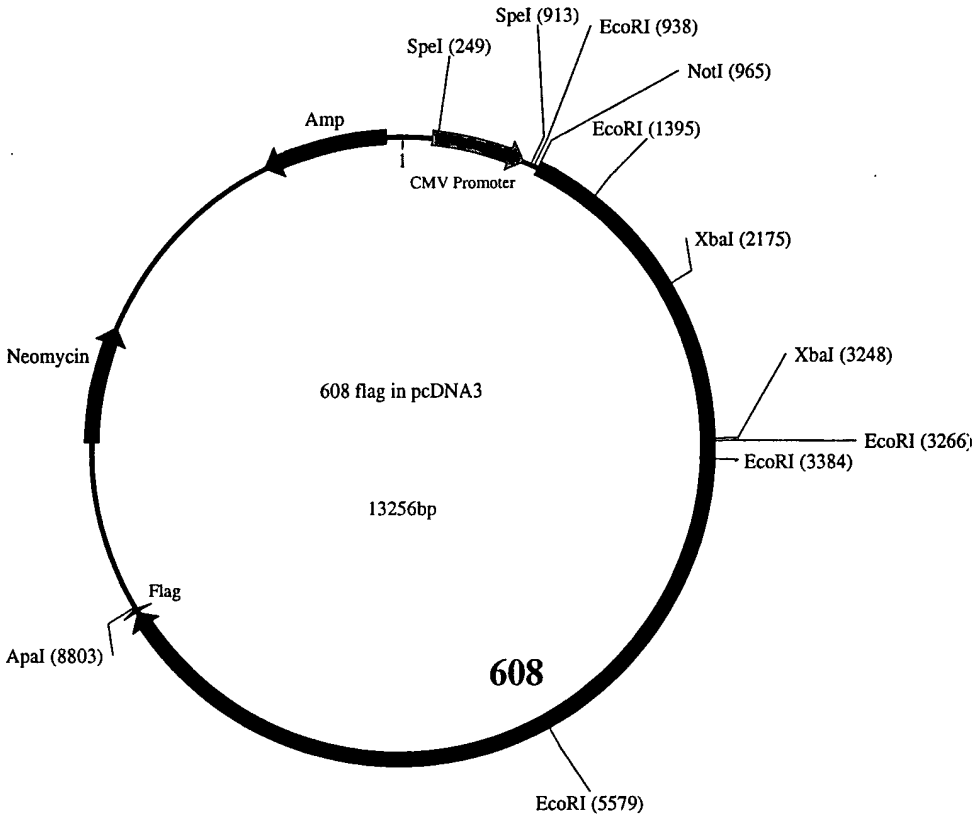
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Figure 3

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Replacement Sheet

Figure 4

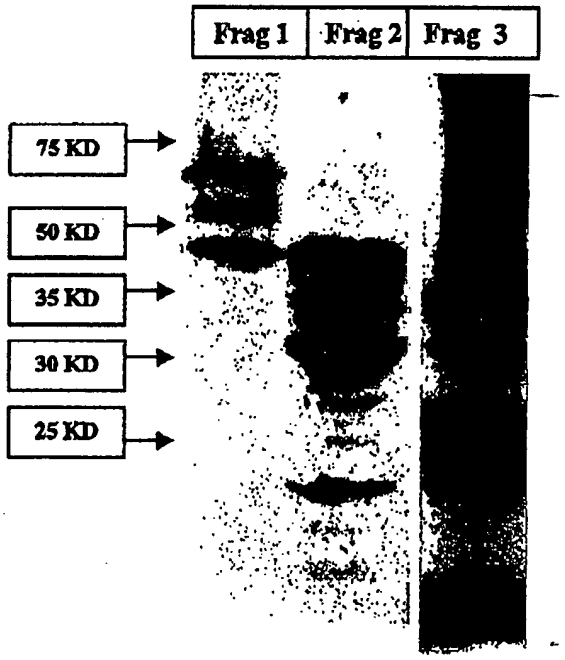


Figure 5

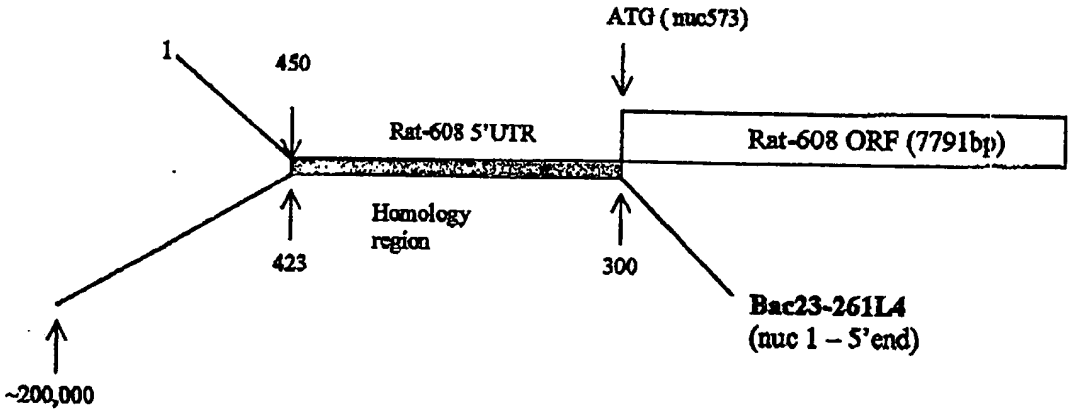


Figure 6

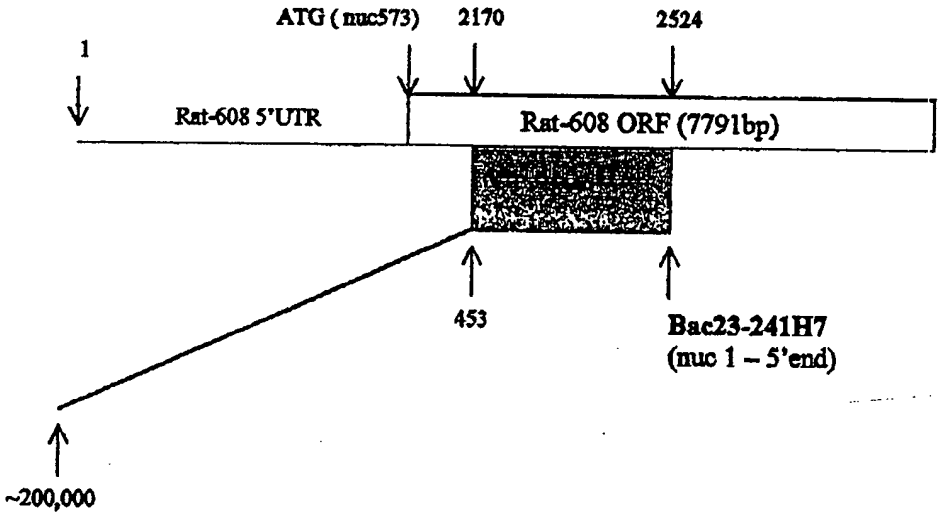
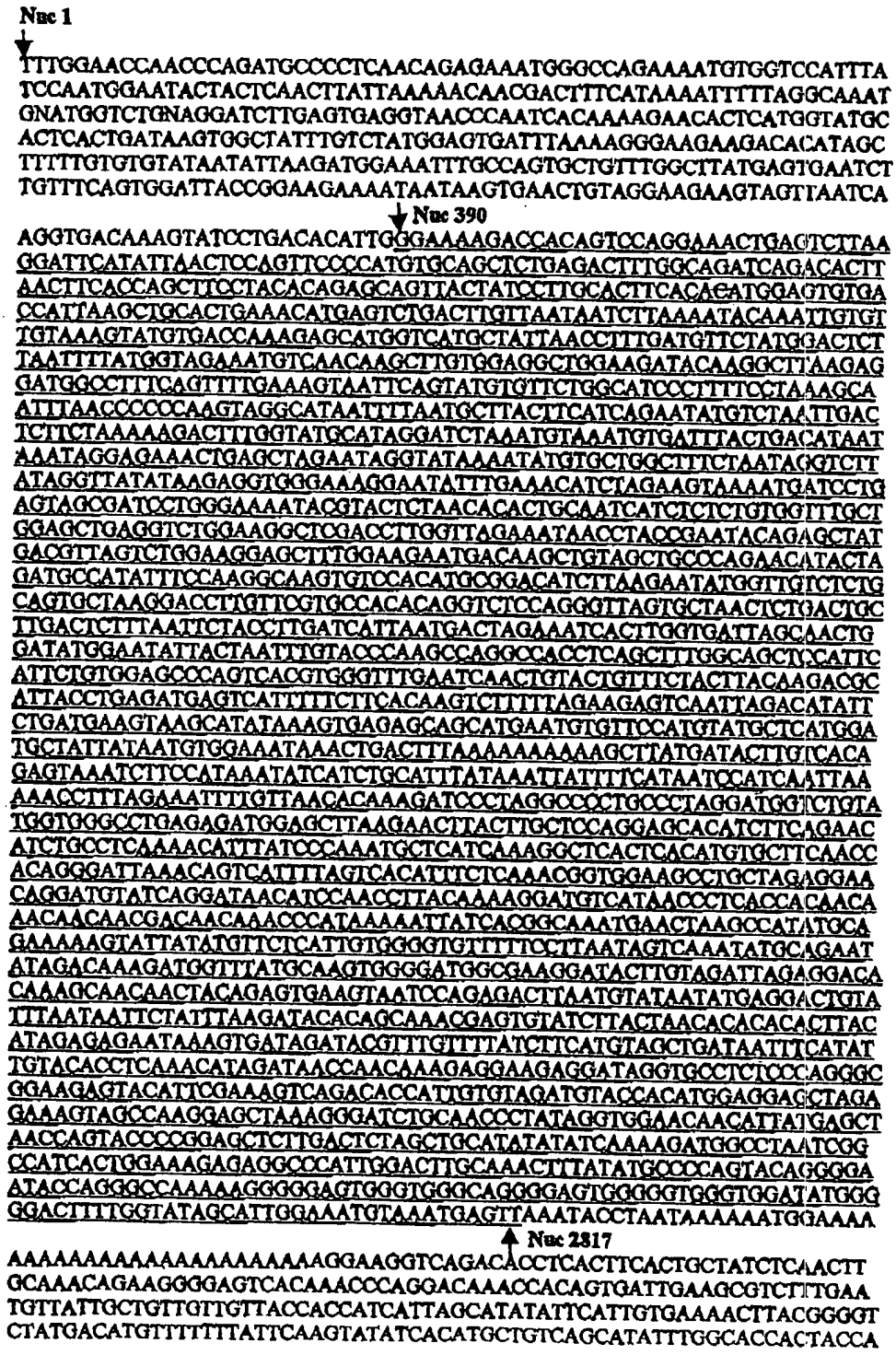
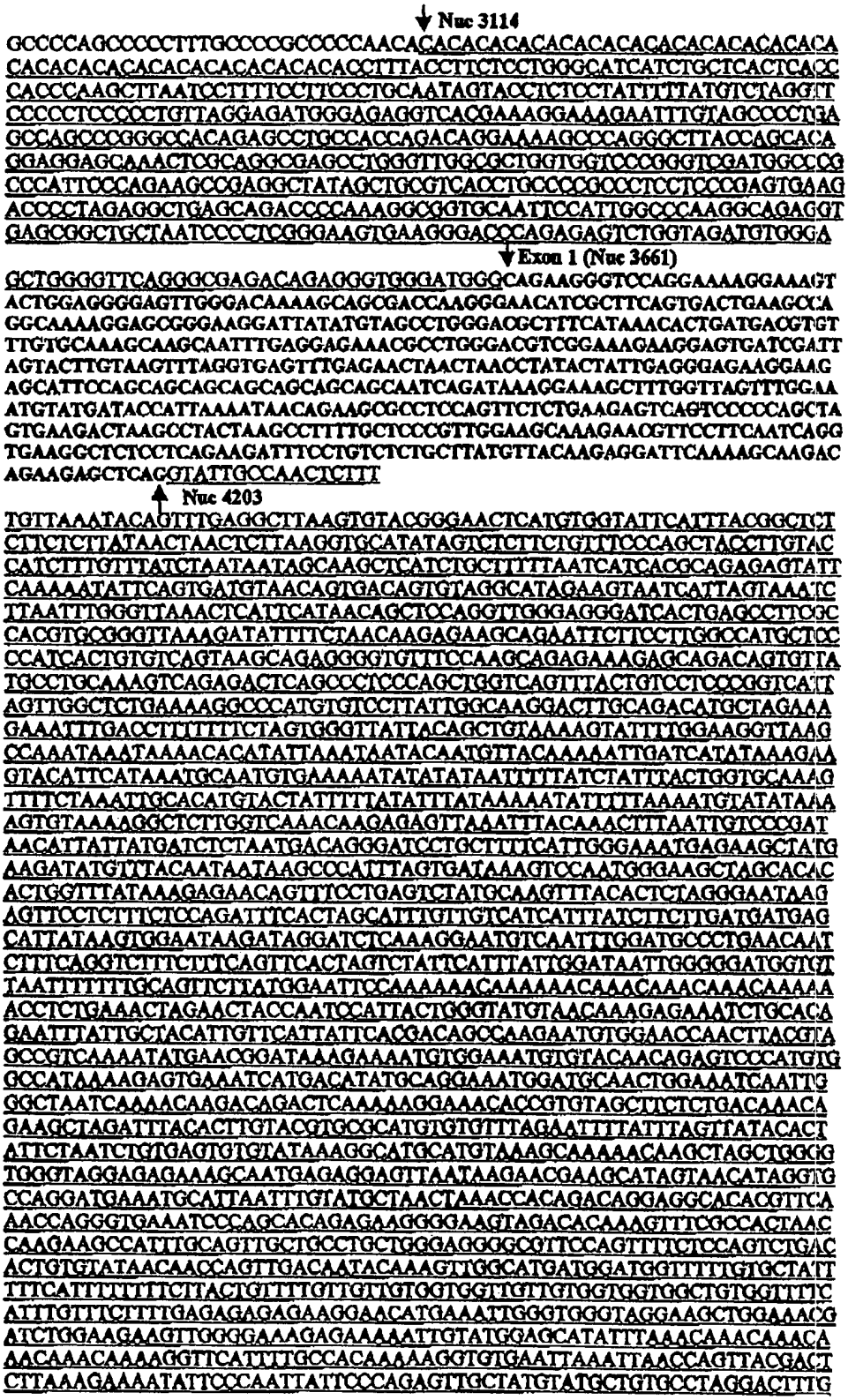


Figure 7

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SUBSTITUTE SHEET (RULE 26)

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(SEQ ID NO:3)

Figure 8

Exon/Intron No.	Exon start	Exon end	Exon length	Intron length
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3	4428	4557	130	3068
4	7625	8019	394	

Figure 9

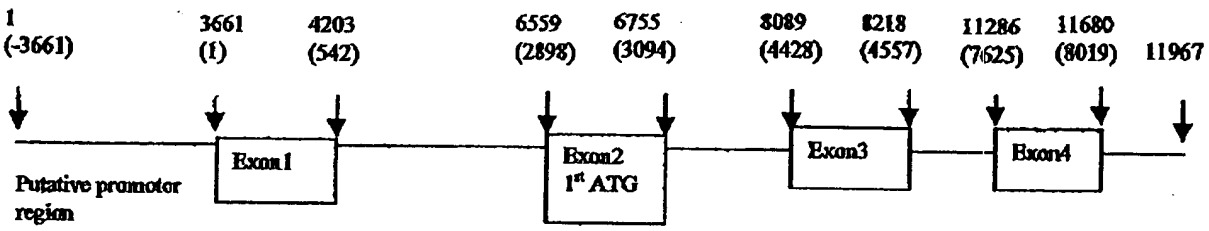
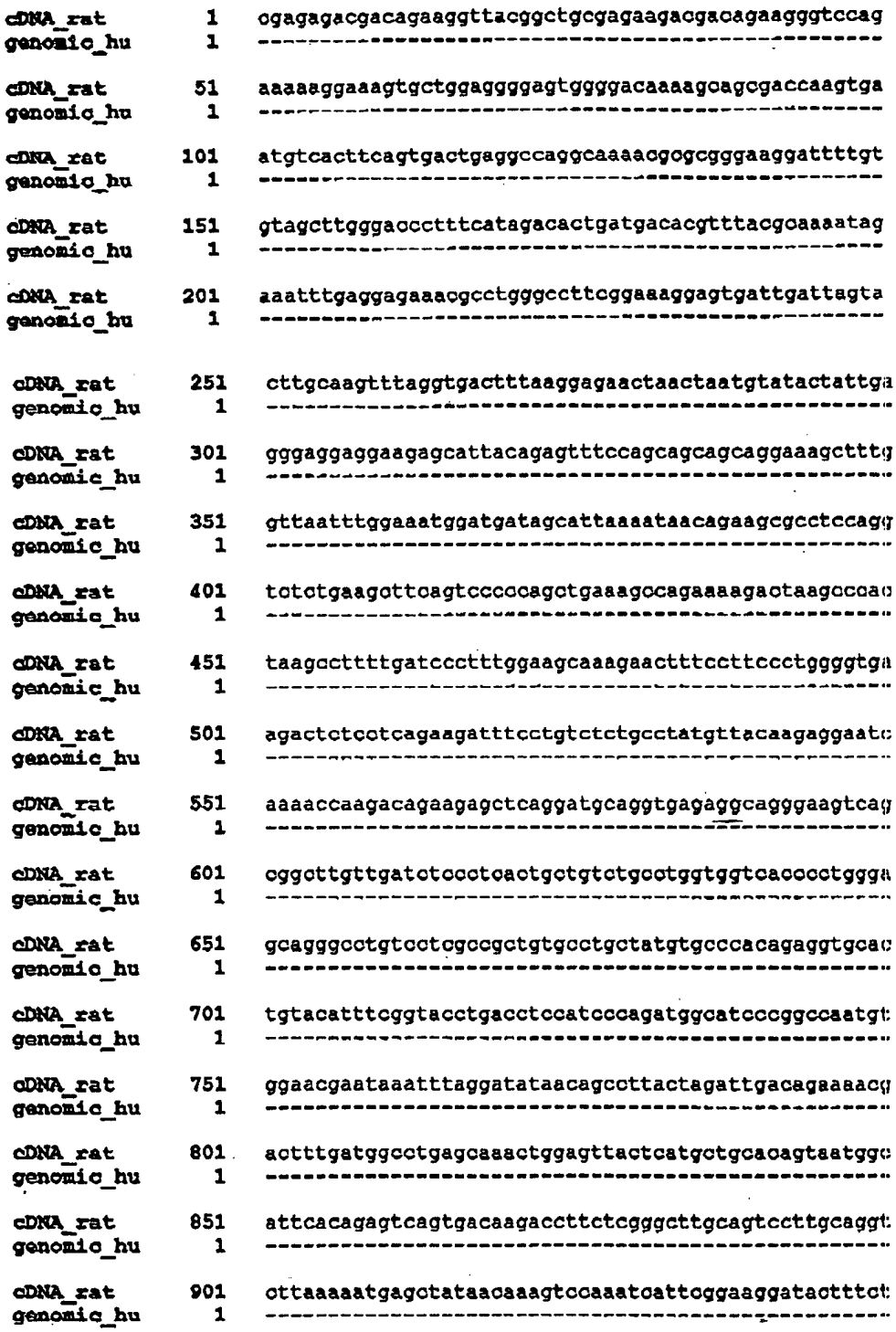


Figure 10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genomic_hu 1 ----------
cDNA_rat 101 atgtcacttcagtgactgaggccaggcaaaacgcgcgggaaggattttgt
genomic_hu 1 ----------
cDNA_rat 151 gtagcttgggaccctttcatagacactgatgacacgtttacgcaaaatag
genomic_hu 1 ----------
cDNA_rat 201 aaatttgaggagaaacgcctgggccttcggaaaggagtgattgattagta
genomic_hu 1 ----------
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genomic_hu 1 ----------
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genomic_hu 1 ----------
cDNA_rat 351 gttaatttggaaatggatgatagcattaaaataacagaagcgcctccagg
genomic_hu 1 ----------
cDNA_rat 401 tctctgaagcttcagtcccccagctgaaagccagaaaagactaagcccac
genomic_hu 1 ----------
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genomic_hu 1 ----------
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genomic_hu 1 ----------
cDNA_rat 901 cttaaaaatgagctataacaaagtccaaatcattcggaaggatactttct
genomic_hu 1 ----------

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genomic_hu      1   ----------------------------------------------------

cDNA_rat     1851   ctttttggttccaacaagaaaaaattgtcttgcagctgaacagaactgcc
genomic_hu      1   ----------------------------------------------------

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genomic_hu       1   ------------------------------------------------

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genomic_hu       1   ------------------------------------------------

cDNA_rat      2201   agctttgatgcaggtctttaccactgcataagcaccaatgatgcagatgc
genomic_hu       1   ------------------------------------------------

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Date Recue/Date Received 2020-05-05

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genomic_hu       1   ------------------------------------------------

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genomic_hu       1   ------------------------------------------------

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cDNA_rat      6101   actccccagcctagtgttcactgggtcctttatgatgggactgaactaaa
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cDNA_rat      6151   accattgcagttgactcattccagatttttcttgtatccaaatggaactc
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genomic_hu       1   ------------------------------------------------
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TGg
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T
A
A
T
C
:
:
t
f
:

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.c_hu    890   CtaTGGAAGCAGAATCACAGTCCATAAAAATGGAACCTTGGAaattagga

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:at     8051   gtgtCAGTGATGGTTGTGGCCTACCCTCCCCGAATCATAAActacctACC
.c_hu   1590   gttcCAGTAATGATTGTAGCCTACCCTCCCCGAATTACAAAtogtccACC

:at     8101   CAGGAACATGCTCAGGAGGACAGGGGAAGCCatgCAGCTCCACTGTGTGG
.c_hu   1640   CAGGAGTATTGTCACCAGGACAGGGGCAGCCtttCAGCTCCACTGTGTGG

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.c_hu   1690   CCTTGGGAGTTCCCAAGCCAgAAATCACATGGGAGATGCCTGACCACTCC

:at     8201   CTGCTCTCAAaagcaacagcaagaaaacccCATAGAAGTGAGATGCTTCA
.c_hu   1740   CTTCTCTCAAcggcaagtaaagagaggacaCATGGAAGTGAGCAGCTTCA

:at     8251   CCCACAAGGTACGCTgGTCATTCAGAATCTCCAAACCTCGGATTCCGGag
.c_hu   1790   CTTACAAGGTACCCTaGTCATTCAGAATCCCCAAACCTCCGATTCTGGga

:at     8301   tcTATAAGTGCAGAGCTCAGAACCTACTTGGgacTGATTACGCAACAACT
.c_hu   1840   taTACAAATGCACAGCAAAGAACCCACTTGGtagTGATTATGCAGCAACG

:at     8351   TACATCCAGGTACTCTGACAGGAAgggggagactaaaattcaacagaagt
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cDNA_rat      8451   TAGGCATGTAAATGAgtcTGAATACATTTACAGTATTAAATTTACAATGG
genomic_hu    1979   TAGGCATGTAAATGAattTGAATACATTTACAGTATTAAATTTACAATGA

cDNA_rat      8501   ACATGCgatga-----GACTTGTAAATGAAAGCATTGTGAACTGAaaccg
genomic_hu    2029   ACATGCaaaataaaagGACTTGTAAATAAATGCATTATGAACTGAtgata

cDNA_rat      8546   agtctctg-----TGGATCTCAAAGCAAACTCTTAACTTAAGGCACTTTg
genomic_hu    2079   ctgatttatttaaTGGATCTCAAAACAAACTTTTAACTTAAGGCACTTTt

cDNA_rat      8591   ATTTTGCCAACAAATAATAACAAACAttaagagaaaaaaatgatcCACTA
genomic_hu    2129   ATTTTGCCAACAAATAACAATAAACAaacattgaaacggtt----CACTA

cDNA_rat      8641   CGAAATAACAAACGGCTAATGCACCTGAATTctcagtaaaaagaccttte
genomic_hu    2175   TAAAATAACAAATGGCTAATGTACCTGAATTtttcagtaaaaaaatgaac

cDNA_rat      8691   tctcgctaacagttgCCAGCTGCCTCGTGTCTGTTTCCTACCAATGTCAC
genomic_hu    2225   ttctaata-------CCAGTTGCCTAGTGTCCACCTCCTATCAATGTTAC

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exon1 (2342-2397)

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cDNA_rat      8829   GTTTATAAACATTTTGATAAAACCGAAAAAAAAAAAAAAaaaaaaaaaaaa
genomic_hu    2360   GTTTATAAATTTTTTTGCTAAAACCTACAGAAAATAAGcactgaactgtc
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(Genomic human OCP: SEQ ID NO:4)
(cDNA rat: SEQ ID NO:5)

Replacement Sheet

Figure 11

Exon/Intron No.	Exon start	Exon end	Exon length	Intron length	Remarks
1	1	208	208	69	No valid splice site found upstream this exon
2	277	429	153	18	
3	447	485	39	1561	
4	2046	2244	199	1351	
5	3595	3724	130	3254	
6	6978	7359	382	4123	
7	11482	14903	3422	38	
8	14941	15307	367	51	
9	15358	15825	468	1039	
10	16864	~17760	~897	?	Last exon might be complete
11	?(1)	2317	~2317	25	Exon is not complete and start site is not known
12	2342	2397	56	-	

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Fig 12.

608 Human translated nucleotide sequence (ORF)

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Figure 13

A

Region						
General	Rat	Human	Region Length	% identity	% positives	% gaps
1-655	1-655	1-653	655	76	86	0
656-726	656-726	654-724	71	46	62	0
727-779	727-779	725-777	53	77	86	0
780-1634	780-1617	778-1612	655	38	53	4
1635-end	1618-end	1613-end	980	74	85	0
	Total	Alignment	2614	62	74	1

B

Region					
Rat	Mouse	Length	% identity	% positives	% gaps
1-238	1-238	238	91	92	1

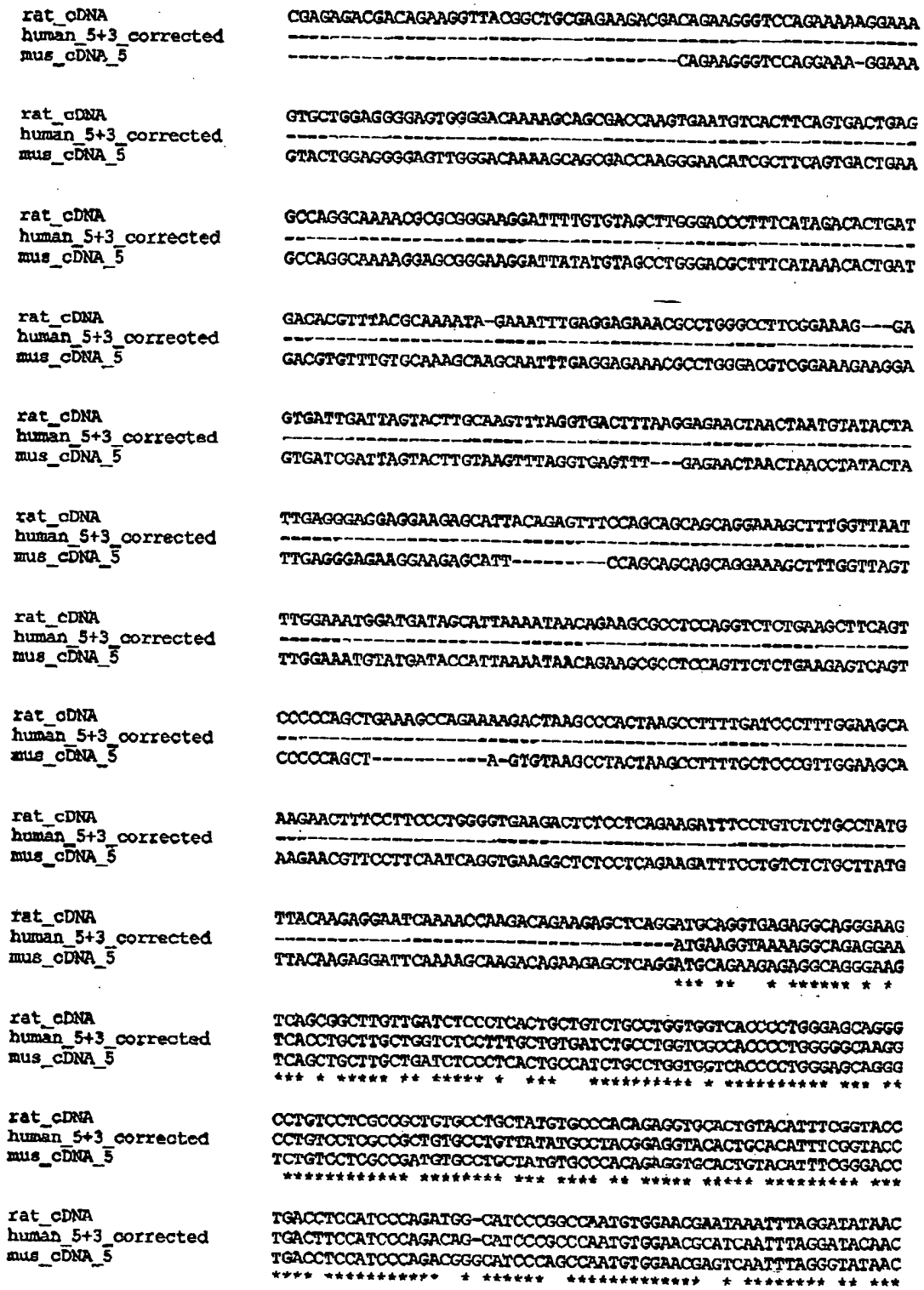
C

Region				
General	Rat	Human	Region Length	% identity
1-1965	1-1965	1-1965	1965	83
1966-2178	1966-2178	1966-2178	213	86
2179-2337	2179-2337	2179-2337	159	86
2338-4893	2338-4893	2338-4863	2565	63
4894-7833	4852-7791	4864-7761	2940	80
	Total	Alignment	7842	80

D

Region				
General	Rat	Mouse	Region Length	% identity
1-720	1-718	1-720	720	93

Figure 14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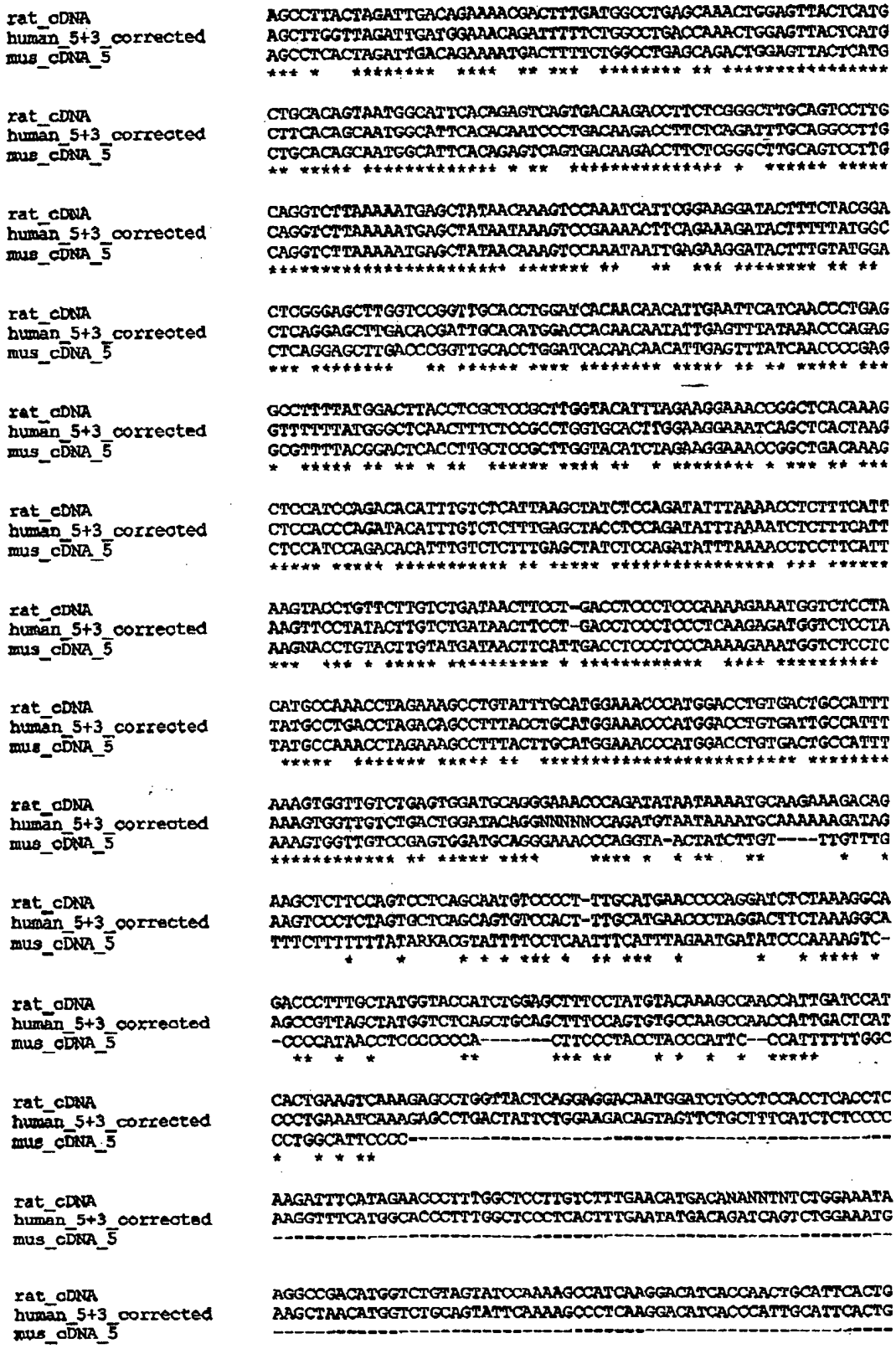
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human_5+3_corrected
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rat_cDNA                ATTATAATCACATCCAGCCAGTGTGGCAACTTCTGGCTTTATACAGTGACTCTCCTCTGA
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mus_cDNA_5              ------------------------------------------------------------

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mus_cDNA_5              ------------------------------------------------------------

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mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                TCCTGGTTGGCGGCACTATTGCCCTGAGCTGTCCAGGCAAAGGCGACCCTTCACCTCACT
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mus_cDNA_5              ------------------------------------------------------------

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mus_cDNA_5              ------------------------------------------------------------

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human_5+3_corrected     TTGGTGAAACACTTGATCTTCCATGCCATTCTACTGGTATCCCAGATGCCTCTATTAGCT
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                GGATTCTTCCAGGGAACACTGTGTTCTCTCAGCCATCAAGAGACAGGCAAATTCTTAACA
human_5+3_corrected     GGGTTATTCCAGGAAACAATGTGCTCTATCAGTCATCAAGAGACAAGAAAGTTCTAAACA
mus_cDNA_5              ------------------------------------------------------------
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rat_cDNA
human_5+3_corrected
mus_cDNA_5
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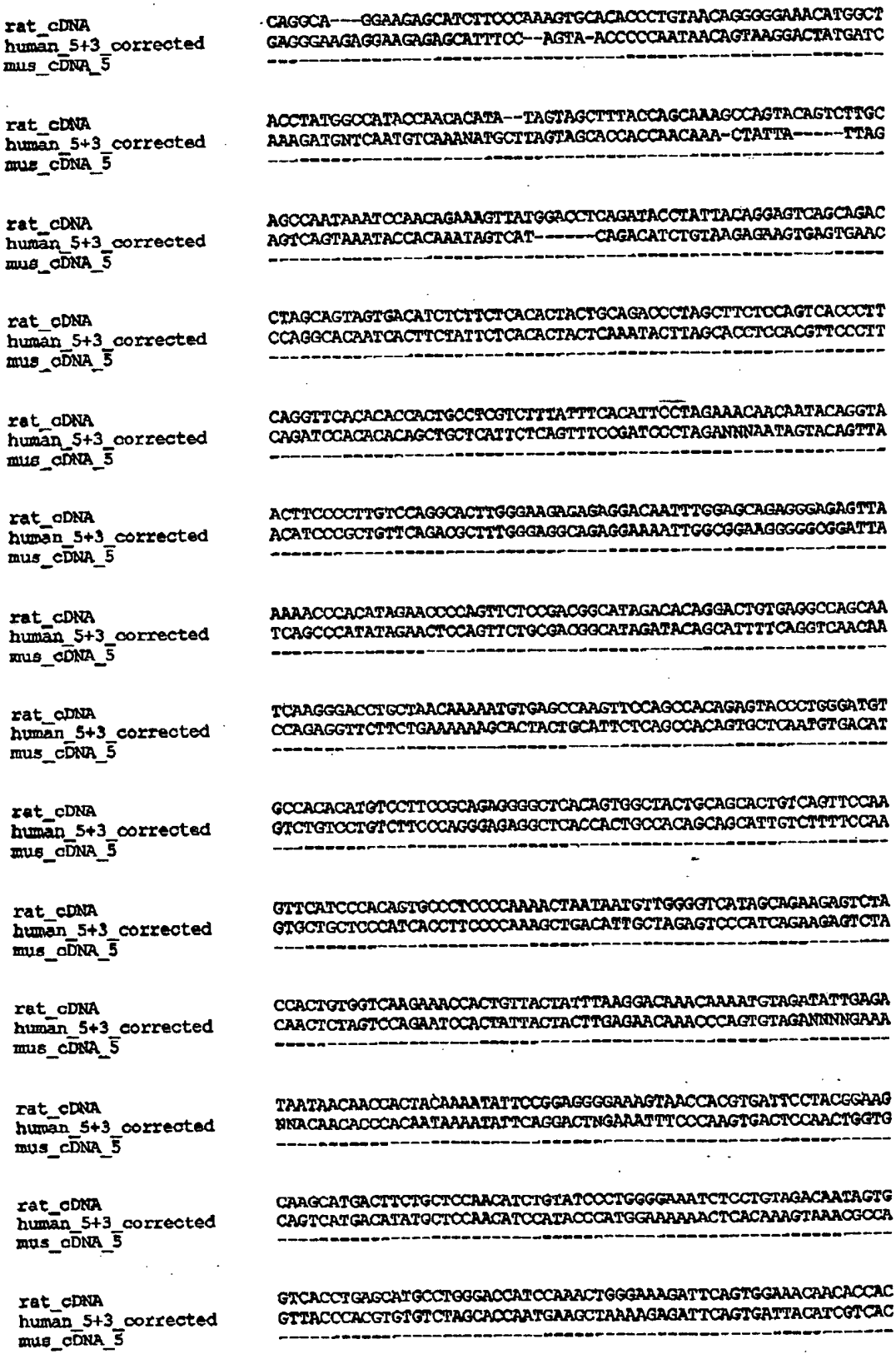
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rat_cDNA
human_5+3_corrected
mus_cDNA_5
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rat_cDNA
human_5+3_corrected
mus_cDNA_5
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Replacement Sheet

rat_cDNA
human_5+3_corrected
mus_cDNA_5
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rat_cDNA                GAGGAGAGAGTGTGTTGGTAGTGCAGTTAGAAGTCCTAGAAATGCTGAGAAGACCAACAT
human_5+3_corrected     GTGGAGAGAGCGTGTTGGTAGTACAGTTAGAAGTACTGGAAATGCTGAGAAGACCGACAT
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                TCAGAAACCCATTCAACGAAAAAGTCATCGCCCAAGCTGGCAAGCCCGTAGCACTGAACT
human_5+3_corrected     TTAGAAATCCATTTAATGAAAAAATAGTTGCCCAGCTGGGAAAGTCCACAGCATTGAATT
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                GCTCTGTGGATGGGAACCCCCCACCTGAAATTACCTGGATCTTACCTGACGGCACACAGT
human_5+3_corrected     GCTCTGTTGATGGTAACCCACCACCTGAAATAATCTGGATTTTACCAAATGGCACACGAT
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                TTGCTAACAGACCACACAATTCCCCGTATCTGATGGCAGGCAATGGCTCTCTCATCCTTT
human_5+3_corrected     TTTCCAATGGACCACAAAGTTATCAGTATCTGATAGCAAGCAATGGTTCTTTTATCATTT
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                ACAAAGCAACTCGGAACAAGTCAGGGAAGTATCGCTGTGCAGCCAGGAATAAGGTTGGCT
human_5+3_corrected     CTAAAACAACTCGGGAGGATGCAGGAAAATATCGCTGTGCAGCTAGGAATAAAGTTGGCT
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                ACATCGAGAAACTCATCCTGTTAGAGATTGGGCAGAAGCCAGTCATTCTGACATACGAAC
human_5+3_corrected     ATATTGAGAAATTAGTCATATTAGAAATTGGCCAGAAGCCAGTTATTCTTACCTATGCAC
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                CAGGGATGGTGAAGAGCGTCAGTGGGGAACCGTTATCACTGCATTGTGTGTCTGATGGGA
human_5+3_corrected     CAGGGACAGTAAAAGGCATCAGTGGAGAATCTCTATCACTGCATTGTGTGTCTGATGGAA
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                TCCCCAAGCCAAATGTCAAGTGGACTACACCGGGTGGCCATGTAATCGACAGGCCTCAAG
human_5+3_corrected     TCCCTAAGCCAAATATCAAATGGACTATGCCAAGTGGTTATGTAGTAGACAGGCCTCAAA
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                TGGATGGAAAATACATACTGCATGAAAATGGCACGCTGGTCATCAAAGCAACAACAGCTC
human_5+3_corrected     TTAATGGGAAATACATATTGCATGACAATGGCACCTTAGTCATTAAAGAAGCAACAGCTT
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                ACGACCAAGGAAATTATATCTGTAGGGCTCAAAACAGTGTTGGCCAGGCAGTTATTAGCG
human_5+3_corrected     ATGACAGAGGAAACTATATCTGTAAGGCTCAAAATAGTGTTGGTCATACACTGATTACTG
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                TGTCAGTGATGGTTGTGGCCTACCCTCCCCGAATCATAAACTACCTACCCAGGAACATGC
human_5+3_corrected     TTCCAGTAATGATTGTAGCCTACCCTCCCCGAATTACAAATCGTCCACCCAGGAGTATTG
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                TCAGGAGGACAGGGGAAGCCATGCAGCTCCACTGTGTGGCCTTGGGAATCCCCAAGCCAA
human_5+3_corrected     TCACCAGGACAGGGGCAGCCTTTCAGCTCCACTGTGTGGCCTTGGGAGTTCCCAAGCCAG
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                AAGTCACCTGGGAGACGCCAAGACACTCCCTGCTCTCAAAAGCAACAGCAAGAAAACCCC
human_5+3_corrected     AAATCACATGGGAGATGCCTGACCACTCCCTTCTCTCAACGGCAAGTAAAGAGAGGACAC
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                ATAGAAGTGAGATGCTTCACCCACAAGGTACGCTGGTCATTCAGAATCTCCAAACCTCGG
human_5+3_corrected     ATGGAAGTGAGCAGCTTCACTTACAAGGTACCCTAGTCATTCAGAATCCCCAAACCTCCG
mus_cDNA_5              ------------------------------------------------------------
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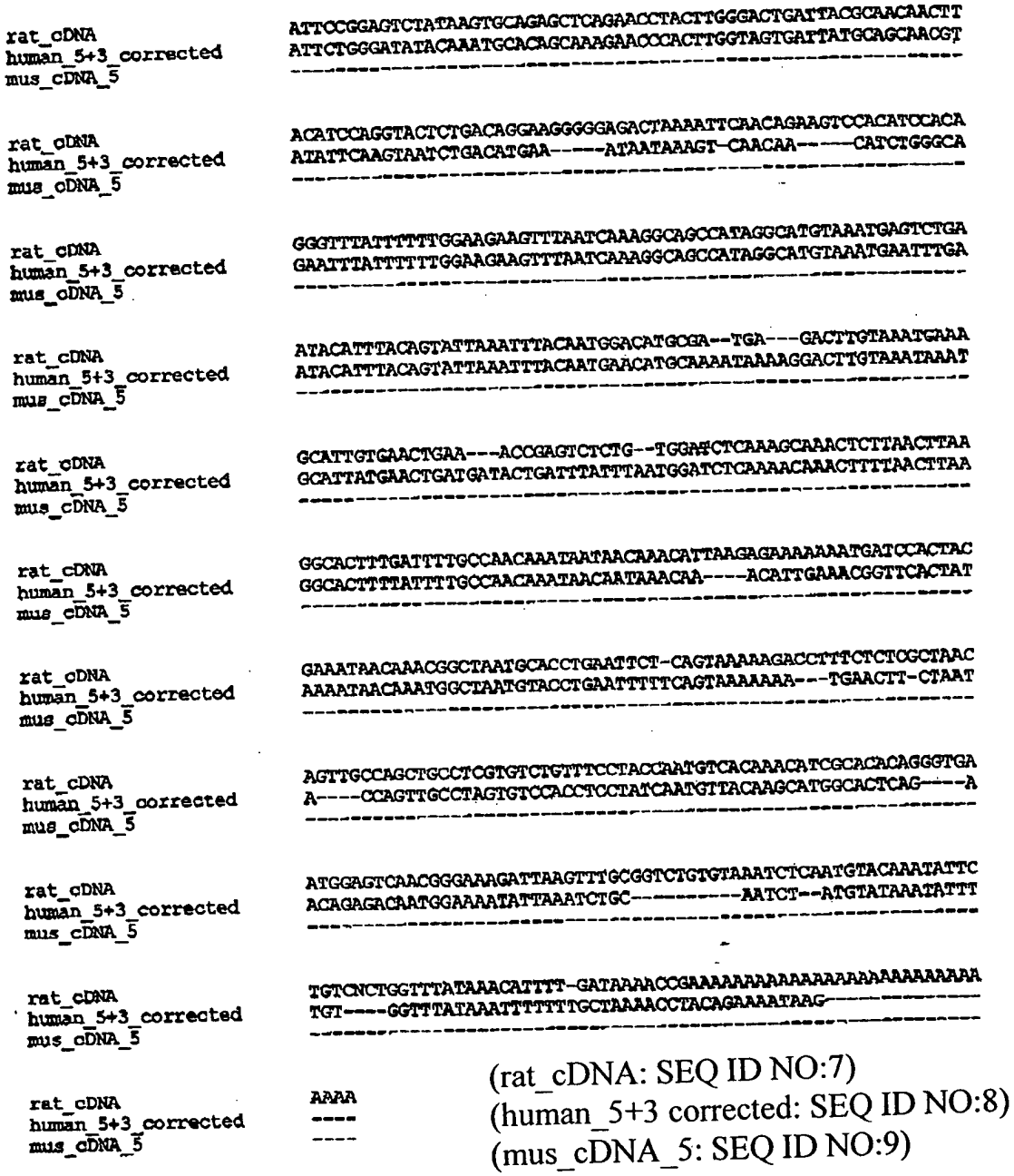
Date Recue/Date Received 2020-10-14



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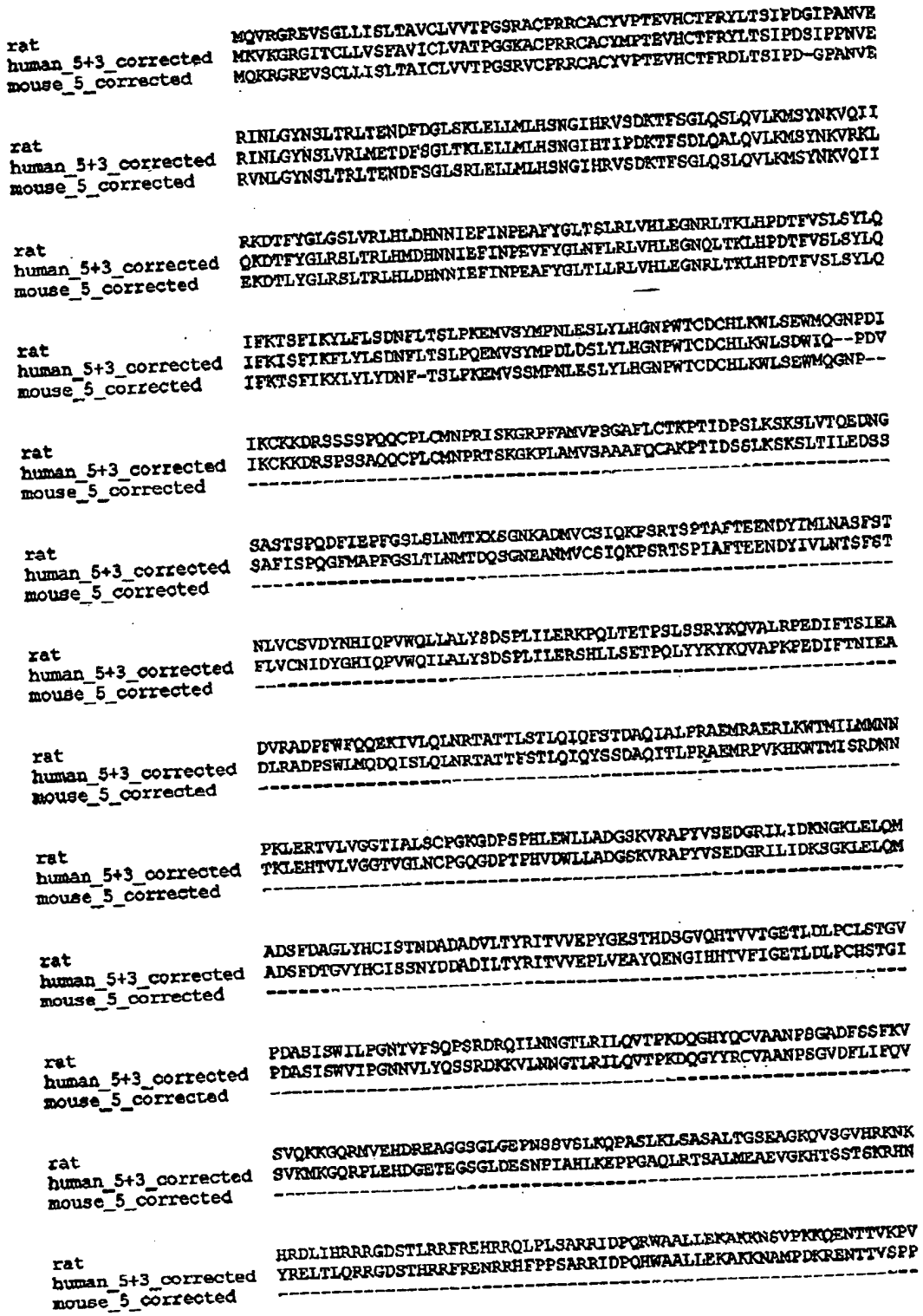
(human_5+3 corrected: SEQ ID NO:8)
(mus_cDNA_5: SEQ ID NO:9)

Figure 15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human_5+3_corrected
mouse_5_corrected
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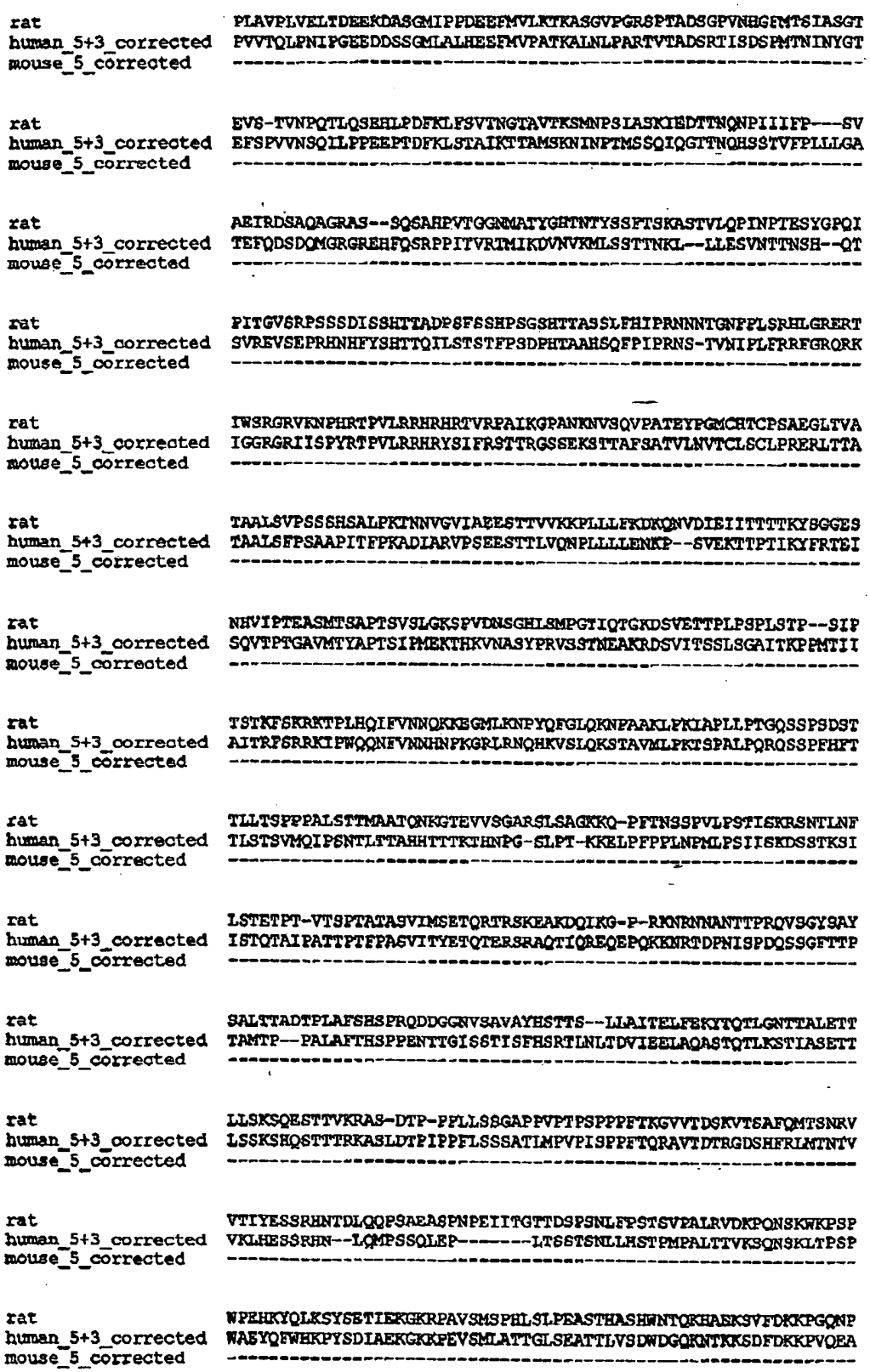
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human_5+3_corrected PVVTQLPNIPGEEDDSSGMLALHEEFMVPATKALNLPARTVTADSRTISDSPMTNINYGT
mouse_5_corrected
rat EVS-TVNPQTLQSEHLPDFKLFSVTNGTAVTKSMNPSLASKIEDTTNQNPIIIFP---SV
human_5+3_corrected EFSPVVNSQILPPEEPTDFKLSTAIKTTAMSKNINPTMSSQIQGTTNQHSSTVFPLLLGA
mouse_5_corrected
rat AEIRDSAQAGRAS--SQSAHPVTGGNMATYGHTNTYSSFTSKASTVLQPINPTESYGPQI
human_5+3_corrected TEFQDSDQMGRGREHFQSRPPITVRIMIKDVNVKMLSSTTNKL--LLESVNTTNSH--QT
mouse_5_corrected
rat PITGVSRPSSSDISSHTTADPSFSSHPSGSHTTASSLFHIPRNNNTGNFPLSRHLGRERT
human_5+3_corrected SVREVSEPRHNHFYSHTTQILSTSTFPSDPHTAAHSQFPIPRNS-TVNIPLFRRFGRQRK
mouse_5_corrected
rat IWSRGRVKNPHRTPVLRRHRHRTVRPAIKGPANKNVSQVPATEYPGMCHTCPSAEGLTVA
human_5+3_corrected IGGRGRIISPYRTPVLRRHRYSIFRSTTRGSSEKSTTAFSATVLNVTCLSCLPRERLTTA
mouse_5_corrected
rat TAALSVPSSSHSALPKTNNVGVIAEESTTVVKKPLLLFKDKQNVDIEIITTTTKYSGGES
human_5+3_corrected TAALSFPSAAPITFPKADIARVPSEESTTLVQNPLLLLENKP--SVEKTTPTIKYFRTEI
mouse_5_corrected
rat NHVIPTEASMTSAPTSVSLGKSPVDNSGHLSMPGTIQTGKDSVETTPLPSPLSTP--SIP
human_5+3_corrected SQVTPTGAVMTYAPTSIPMEKTHKVNASYPRVSSTNEAKRDSVITSSLSGAITKPPMTII
mouse_5_corrected
rat TSTKFSKRKTPLHQIFVNNQKKSGMLKNPYQFGLQKNPAAKLPKIAPLLPTGQSSPSDST
human_5+3_corrected AITRFSRRKIPWQQNFVNNHNPKGRLRNQHKVSLQKSTAVMLPKTSPALPQRQSSPFHFT
mouse_5_corrected
rat TLLTSPPPALSTTMAATQNKGTEVVSGARSLSAGKKQ-PFTNSSPVLPSTISKRSNTLNF
human_5+3_corrected TLSTSVMQIPSNTLTTAHHTTTKTHNPG-SLPT-KKELPFPPLNPMLPSIISKDSSTKSI
mouse_5_corrected
rat LSTETPT-VTSPTATASVIMSETQRTRSKEAKDQIKG-P-RKNRNNANTTPRQVSGYSAY
human_5+3_corrected ISTQTAIPATTPTFPASVITYETQTERSRAQTIQREQEPQKENRTDPNISPDQSSGFTTP
mouse_5_corrected
rat SALTTADTPLAFSHSPRQDDGGNVSAVAYHSTTS--LLAITELFEKITQTLGNTTALETT
human_5+3_corrected TAMTP--PALAFTHSPPENTTGISSTISFHSRTLNLTDVIEELAQASTQTLKSTIASETT
mouse_5_corrected
rat LLSKSQESTTVKRAS-DTP-PFLLSSGAPPVPTPSPPPFTKGVVTDSKVTSAFQMTSNRV
human_5+3_corrected LSSKSHQSTTTRKASLDTPIPPFLSSSATIMPVPISPPFTQRAVTDTRGDSHFRLMTNTV
mouse_5_corrected
rat VTIYESSRHNTDLQQPSAEASPNPEIITGTTDSPSNLFPSTSVPALRVDKPQNSKWKPSP
human_5+3_corrected VKLHESSRHN--LQMPSSQLEP-------LTSSTSNLLHSTPMPALTTVKSQNSKLTPSP
mouse_5_corrected
rat WPEHKYQLKSYSETIEKGKRPAVSMSPHLSLPEASTHASHWNTQKHAEKSVFDKKPGQNP
human_5+3_corrected WAEYQFWHKPYSDIAEKGKKPEVSMLATTGLSEATTLVSDWDGQKNTKKSDFDKKPVQEA
mouse_5_corrected

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human_5+3_corrected     TTSKLLPFDSLSRYIFEKPRIVGGKAASFTIPANSDAFLPCEAVGNPLPTIHWTRVS-GL
mouse_5_corrected       ------------------------------------------------------------

rat                     EISQGTQKSRFHVLPNGTLSIQRVSIQDRGQYLCSAFNPLGVDHFHVSLSVVFYPARILD
human_5+3_corrected     DLSRGNQNSRVQVLPNGTLSIQRVEIQDRGQYLCSASNLFGTDHLHVTLSVVSYPPRILE
mouse_5_corrected       ------------------------------------------------------------

rat                     RHVKEITVHFGSTVELKCRVEGMPRPTVSWILANQTVVSETAKGSRKVWVTPDGTLIIYN
human_5+3_corrected     RRTKEITVHSGSTVELKCRAEGRPSPTVTWILANQTVVSESSQGSRQAVVTVDGTLVLHN
mouse_5_corrected       ------------------------------------------------------------

rat                     LSLYDRGFYKCVASNPSGQDSLLVKIQVITAPPVIIEQKRQAIVGVLGGSLKLPCTAKGT
human_5+3_corrected     LSIYDRGFYKCVASNPGGQDSLLVKIQVIAAPPVILEQRRQVIVGTWGESLKLPCTAKGT
mouse_5_corrected       ------------------------------------------------------------

rat                     PQPSVHWVLYDGTELKPLQLTHSRFFLYPNGTLYIRSIAPSVRGTYECIATSSSGSERRV
human_5+3_corrected     PQPSVYWVLSDGTEVKPLQFTNSKLFLFSNGTLYIRNLASSDRGTYECIATSSTGSERRV
mouse_5_corrected       ------------------------------------------------------------

rat                     VILTVEEGETIPRIETASQKWTEVNLGEKLLLNCSATGDPKPRIIWRLPSKAVIDQWHRM
human_5+3_corrected     VMLTMEERVTSPRIEAASQKRTEVNFGDKLLLNCSATGEPKPQIMWRLPSKAVVDQ----
mouse_5_corrected       ------------------------------------------------------------

rat                     GSRIHVYPNGSLVVGSVTEKDAGDYLCVARNKMGDDLVLMHVRLRLTPAKIEQKQYFKKQ
human_5+3_corrected     GSWIHVYPNGSLFIGSVTEKDSGVYLCVARNKMGDDLILMHVSLRLKPAKIDHKQYFRKQ
mouse_5_corrected       ------------------------------------------------------------

rat                     VLHGKDFQVDCKASGSPVPEVSWSLPDGTVLNNVAQADDSGYRTKRYTLFHNGTLYFNNV
human_5+3_corrected     VLHGKDFQVDCKASGSPVPEISWSLPDGTNINNAMQADDSGHRTRRYTLFNNGTLYFNKV
mouse_5_corrected       ------------------------------------------------------------

rat                     GMAEEGDYICSAQNTLGKDEMKVHLTVLTAIPRIRQSYKTTMRLRAGETAVLDCEVTGEP
human_5+3_corrected     GVAEEGDYTCYAQNTLGKDEMKVHLTVITAAPRIRQSNKTNKRIKAGDTAVLDCEVTGDP
mouse_5_corrected       ------------------------------------------------------------

rat                     KPNVFWLLPSNNVISFSNDRFTFHANRTLSIHKVKPLDSGDYVCVAQNPSGDDTKTYKLD
human_5+3_corrected     KPKIFWLLPSNDMISFSIDRYTFHANGSLTINKVKLLDSGEYVCVARNPSGDDTKMYKLD
mouse_5_corrected       ------------------------------------------------------------

rat                     IVSKPPLINGLYANKTVIKATAIRHSKKYFDCRADGIPSSQVTWIMPGNIFLPAPYFGSR
human_5+3_corrected     VVSKPPLINGLYTNRTVIKATAVRHSKKHFDCRAEGTPSPEVMWIMPDNIFLTAPYYGSR
mouse_5_corrected       ------------------------------------------------------------

rat                     VTVHPNGTLEMRNIRLSDSADFTCVVRSEGGESVLVVQLEVLEMLRRPTFRNPFNEKVIA
human_5+3_corrected     ITVHKNGTLEIRNVRLSDSADFICVARNEGGESVLVVQLEVLEMLRRPTFRNPFNEKIVA
mouse_5_corrected       ------------------------------------------------------------

rat                     QAGKPVALNCSVDGNPPPEITWILPDGTQFANRPHNSPYIMAGNGSLILYKATRNKSGKY
human_5+3_corrected     QLGKSTALNCSVDGNPPPEIIWILPNGTRFSNGPQSYQYLIASNGSFIISKTTREDAGKY
mouse_5_corrected       ------------------------------------------------------------

rat                     RCAARNKVGYIEKLILLEIGQKPVILTYPPGMVKSVSGEPLSLHCVSDGIPKPNVKWTTP
human_5+3_corrected     RCAARNKVGYIEKLVILEIGQKPVILTYAPGTVKGISGESLSLHCVSDGIPKPNIKWTMP
mouse_5_corrected       ------------------------------------------------------------
```

```
rat                   GGHVIDRPQVDGKYILHENGTLVIKATTAHDQGNYICRAQNSVGQAVISVSVMVVAIPPR
human_5+3_corrected   SGYVVDRPQINGKYILHDNGTLVIKEATAYDRGNYICKAQNSVGHTLITVPVMIVAYPPR
mouse_5_corrected     ------------------------------------------------------------

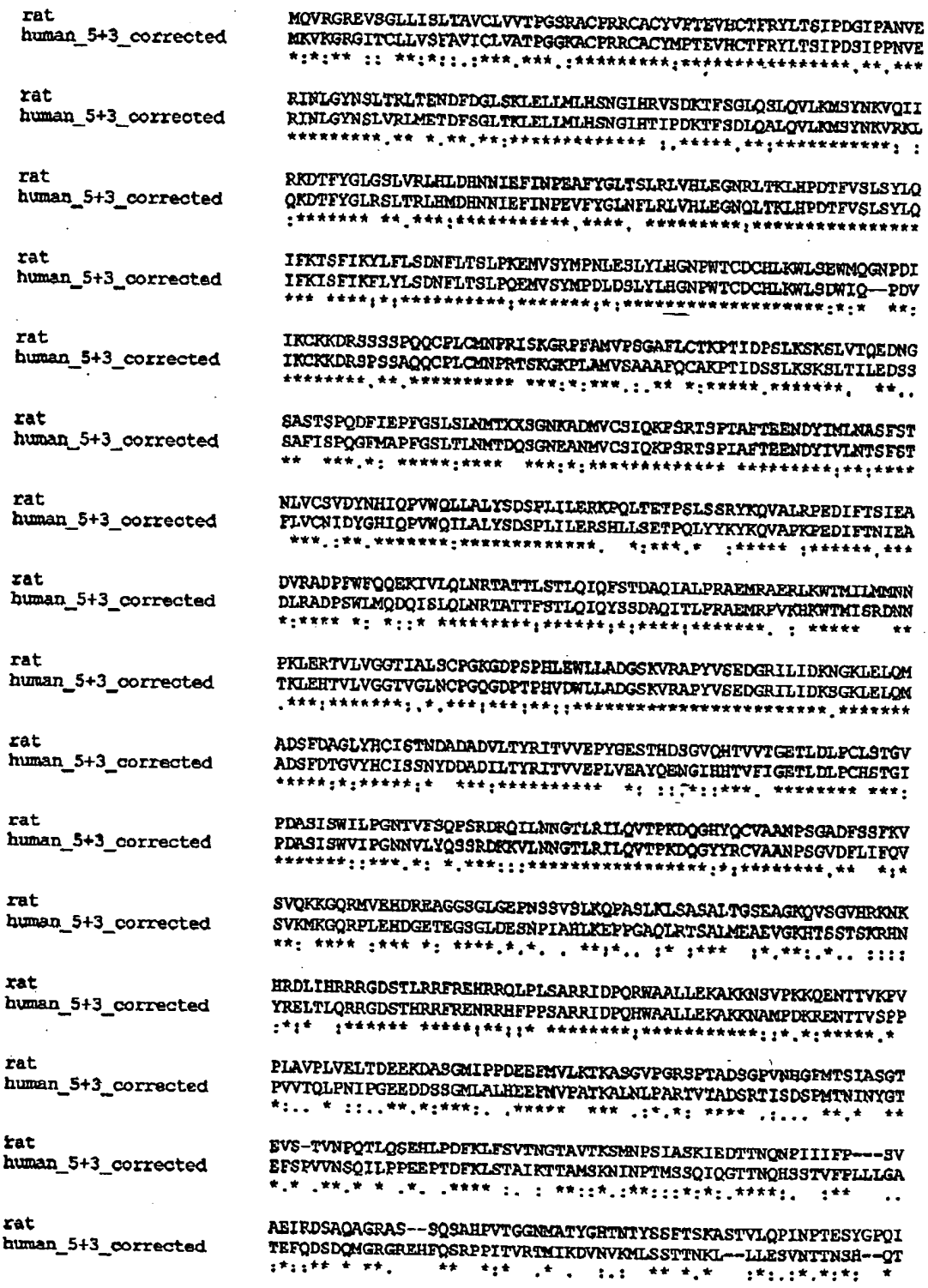
rat                   IINYLPRNMLRRTGEANQLHCVALGIPKPKVTWETPRHSLLSKATARKPHRSEMLHPQGT
human_5+3_corrected   ITNRPPRSIVTRTGAAPQLHCVALGVPKPEITWEMPDHSLLSTASKERTHGSEQLHLQGT
mouse_5_corrected     ------------------------------------------------------------

rat                   LVIQNLQTSDSGVYKCRAQNLLGTDYATTYIQV
human_5+3_corrected   LVIQNPQTSDSGIYKCTAKNPLGSDYAATYIQV
mouse_5_corrected     -------------------------------
```

(rat: SEQ ID NO:10)
(human_5+3_corrected: SEQ ID NO:11)
(mouse_5_corrected: SEQ ID NO:12)

Jul 12, 2005 10:30:14 AM

Figure 16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rat
human_5+3_corrected
RINLGYNSLTRLTENDFDGLSKLELLMLHSNGIHRVSDKTFSGLQSLQVLKMSYNKVQII
RINLGYNSLVRLMETDFSGLTKLELLMLHSNGIHTIPDKTFSDLQALQVLKMSYNKVRKL
rat
human_5+3_corrected
RKDTFYGLGSLVRLHLDHNNIEFINPEAFYGLTSLRLVHLEGNRLTKLHPDTFVSLSYLQ
QKDTFYGLRSLTRLHMDHNNIEFINPEVFYGLNFLRLVHLEGNQLTKLHPDTFVSLSYLQ
rat
human_5+3_corrected
IFKTSFIKYLFLSDNFLTSLPKEMVSYMPNLESLYLHGNPWTCDCHLKWLSEWMQGNPDI
IFKISFIKFLYLSDNFLTSLPQEMVSYMPDLDSLYLHGNPWTCDCHLKWLSDWIQ—PDV
rat
human_5+3_corrected
IKCKKDRSSSSPQQCPLCMNPRISKGRPFAMVPSGAFLCTKPTIDPSLKSKSLVTQEDNG
IKCKKDRSPSSAQQCPLCMNPRTSKGKPLAMVSAAAFQCAKPTIDSSLKSKSLTILEDSS
rat
human_5+3_corrected
SASTSPQDFIEPFGSLSLNMTXXSGNKADMVCSIQKPSRTSPTAFTEENDYIMLNASFST
SAFISPQGFMAPFGSLTLNMTDQSGNEANMVCSIQKPSRTSPIAFTEENDYIVLNTSFST
rat
human_5+3_corrected
NLVCSVDYNHIQPVWQLLALYSDSPLILERKPQLTETPSLSSRYKQVALRPEDIFTSIEA
FLVCNIDYGHIQPVWQILALYSDSPLILERSHLLSETPQLYYKYKQVAPKPEDIFTNIEA
rat
human_5+3_corrected
DVRADPFWFQQEKIVLQLNRTATTLSTLQIQFSTDAQIALPRAEMRAERLKWTMILMMNN
DLRADPSWLMQDQISLQLNRTATTFSTLQIQYSSDAQITLPRAEMRPVKHKWTMISRDNN
rat
human_5+3_corrected
PKLERTVLVGGTIALSCPGKGDPSPHLEWLLADGSKVRAPYVSEDGRILIDKNGKLELQM
TKLEHTVLVGGTVGLNCPGQGDPTPHVDWLLADGSKVRAPYVSEDGRILIDKSGKLELQN
rat
human_5+3_corrected
ADSFDAGLYHCISTNDADADVLTYRITVVEPYGESTHDSGVQHTVVTGETLDLPCLSTGV
ADSFDTGVYHCISSNYDDADILTYRITVVEPLVEAYQENGIHHTVFIGETLDLPCHSTGI
rat
human_5+3_corrected
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PDASISWVIPGNNVLYQSSRDKKVLNNGTLRILQVTPKDQGYYRCVAANPSGVDFLIFQV
rat
human_5+3_corrected
SVQKKGQRMVEHDREAGGSGLGEPNSSVSLKQPASLKLSASALTGSEAGKQVSGVHRKNK
SVKMKGQRPLEHDGETEGSGLDESNPIAHLKEPPGAQLRTSALMEAEVGKHTSSTSKRHN
rat
human_5+3_corrected
HRDLIHRRRGDSTLRRFREHRRQLPLSARRIDPQRWAALLEKAKKNSVPKKQENTTVKPV
YRELTLQRRGDSTHRRFRENRRHFPPSARRIDPQHWAALLEKAKKNAMPDKRENTTVSPP
rat
human_5+3_corrected
PLAVPLVELTDEEKDASGMIPPDEEEFMVLKTKASGVPGRSPTADSGPVNHGFMTSIASGT
PVVTQLPNIPGEEDDSSGMLALHEEFNVPATKALNLPARTVTADSRTISDSPMTNINYGT
rat
human_5+3_corrected
EVS-TVNPQTLQSEHLPDFKLFSVTNGTAVTKSMNPSIASKIEDTTNQNPIIIFP---SV
EFSPVVNSQILPPEEPTDFKLSTAIKTTAMSKNINPTMSSQIQGTTNQHSSTVFPLLLGA
rat
human_5+3_corrected
AEIRDSAQAGRAS--SQSAHPVTGGNMATYGHTNTYSSFTSKASTVLQPINPTESYGPQI
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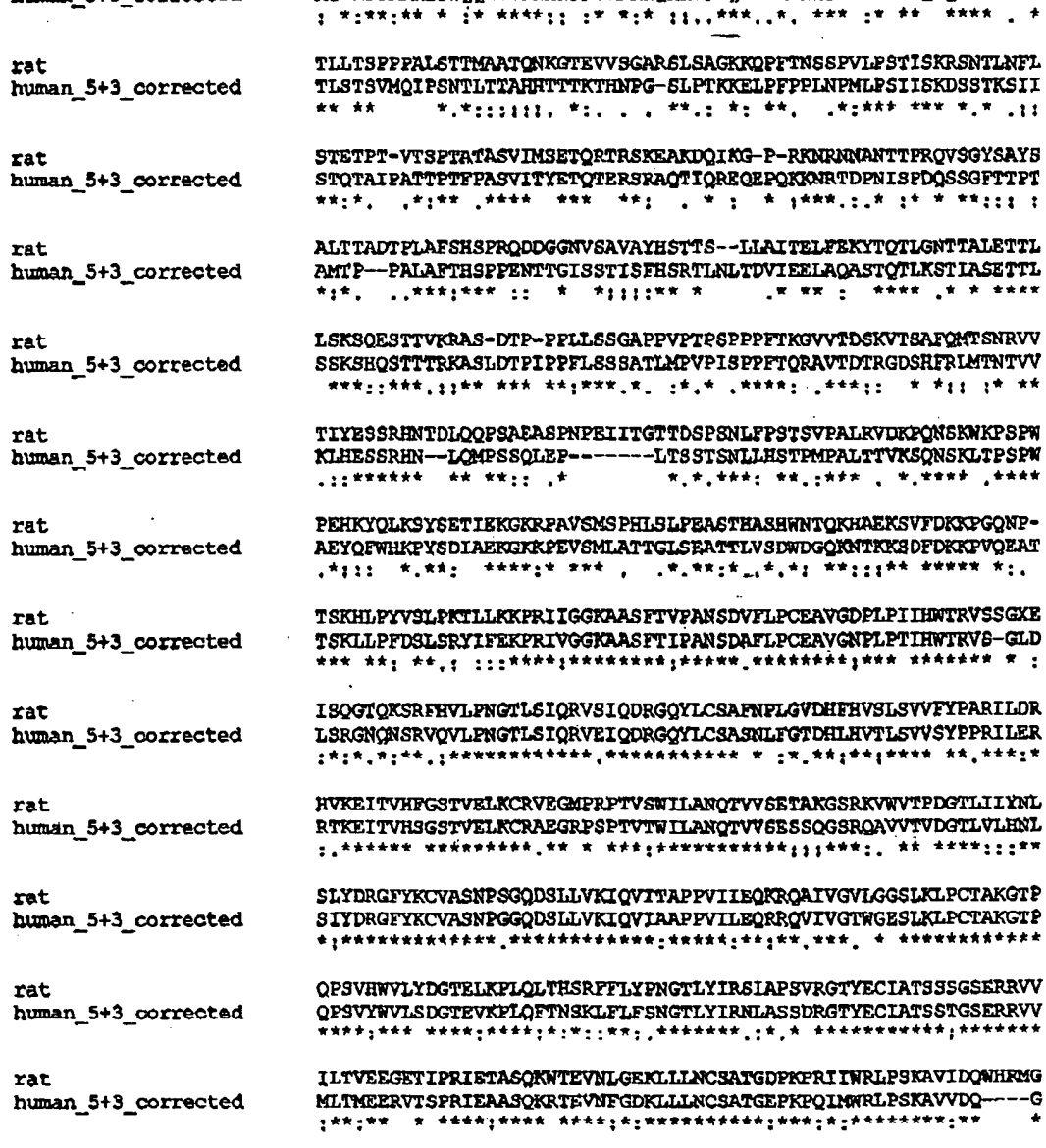
rat
human_5+3_corrected
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IGGRGRIISPYRTPVLRRHRYSIFRSTTRGSSEKSTTAFSATVLNVTCLSCLPRERLTTA
TAALSVPSSSHSALPKTNNVGVIAEESTTVVKKPLLLFKDKQNVDIEIITTTTKYSGGES
TAALSFPSAAPITFPKADIARVPSEESTTLVQNPLLLLENKP--SVEKTTPTIKYFRTEI
NHVIPTEASMTSAPTSVSLGKSPVDNSGHLSMPGTIQTGKDSVETTPLPSPLSTP--SIP
SQVTPTGAVMTYAPTSIPMEKTHKVNASYPRVSSTNEAKRDSVITSSLSGAITKPPMTII
TSTKFSKRKTPLHQIFVNNQKKEGMLKNPYQFGLQKNPAAKLPKIAPLLPTGQSSPSDST
AITRFSRRKIPWQQNFVNNHNPKGRLRNQHKVSLQKSTAVMLPKTSPALPQRQSSPFHFT
TLLTSPPPALSTTMAATQNKGTEVVSGARSLSAGKKQPFTNSSPVLPSTISKRSNTLNFL
TLSTSVMQIPSNTLTTAHHTTTKTHNPG-SLPTKKELPFPPLNPMLPSIISKDSSTKSII
STETPT-VTSPTATASVIMSETQRTRSKEAKDQIKG-P-RKNRNNANTTPRQVSGYSAYS
STQTAIPATTPTFPASVITYETQTERSRAQTIQREQEPQKQNRTDPNISPDQSSGFTTPT
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AMTP---PALAFTHSPPENTTGISSTISFHSRTLNLTDVIEELAQASTQTLKSTIASETTL
LSKSQESTTVKRAS-DTP-PPLLSSGAPPVPTPSPPPFTKGVVTDSKVTSAFQMTSNRVV
SSKSHQSTTTRKASLDTPIPPPFLSSSATLMPVPISPPFTQRAVTDTRGDSRFRLMTNTVV
TIYESSRHNTDLQQPSAEASPNPELITGTTDSPSNLFPSTSVPALRVDKPQNSKWKPSPW
KLHESSRHN--LQMPSSQLEP-------LTSSTSNLLHSTPMPALTTVKSQNSKLTPSPW
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AEYQFWHKPYSDIAEKGKKPEVSMLATTGLSEATTLVSDWDGQKNTKKSDFDKKPVQEAT
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TSKLLPFDSLSRYIFEKPRIVGGKAASFTIPANSDAFLPCEAVGNPLPTIHWTRVS-GLD
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LSRGNQNSRVQVLPNGTLSIQRVEIQDRGQYLCSASNLFGTDHLHVTLSVVSYPPRILER
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RTKEITVHSGSTVELKCRAEGRPSPTVTWILANQTVVSESSQGSRQAVVTVDGTLVLHNL
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ILTVEEGETIPRIETASQKWTEVNLGEKLLLNCSATGDPKPRIIWRLPSKAVIDQWHRMG
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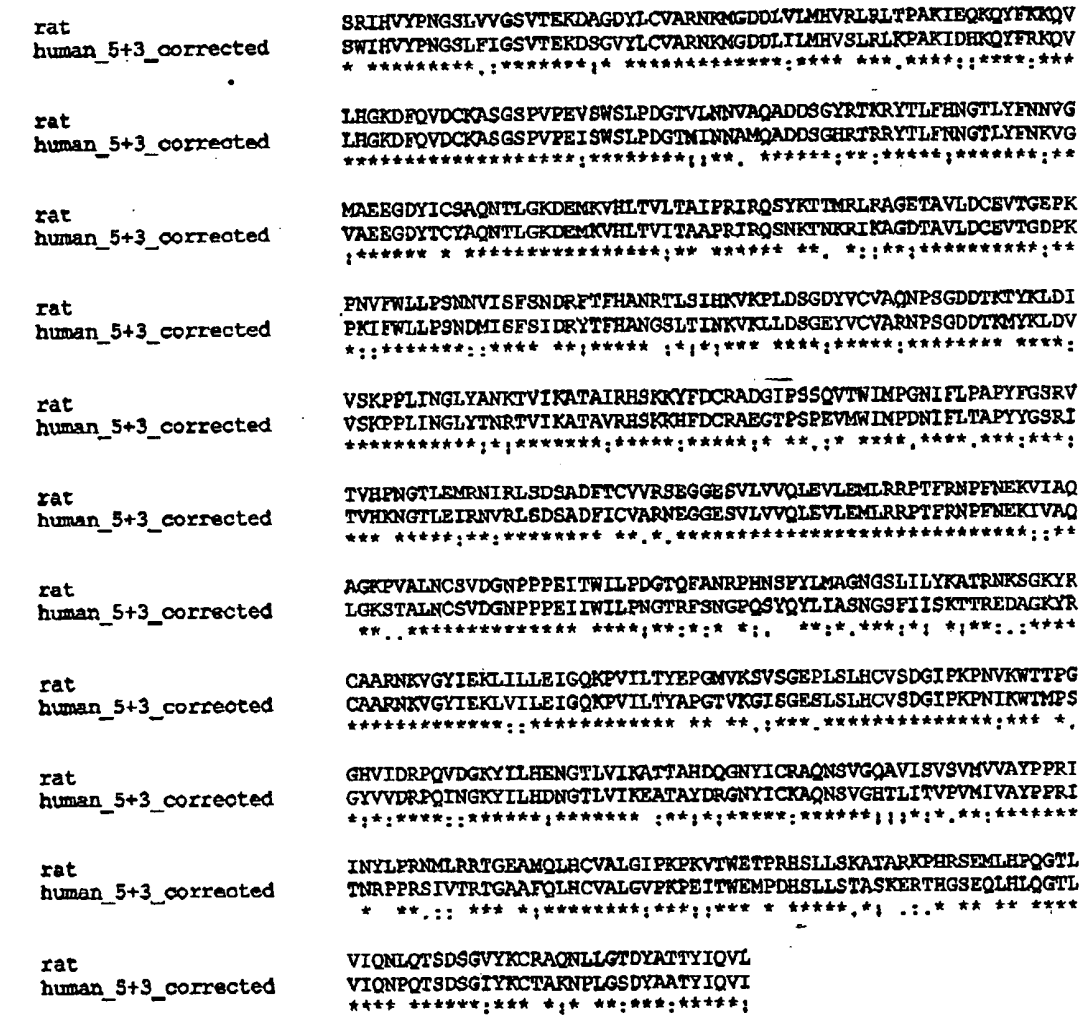

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(human_5+3_corrected: SEQ ID NO:14)

Figure 17

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(SEQ ID NO: 15)

Figure 18

MKVKGRGITCLLVSFAVICLVATPGGKACPRRCACYMPTEVHCTFRYLTSIPDSIPPNVE
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LQKDTFYGLRSLTRLHMDHNNIEFINPEVFYGLNFLRLVHLEGNQLTKLHPDTFVSLSYL
QIFKISFIKFLYLSDNFLTSLPQEMSYMPDLDSLLYLHGNPWTCDCHLRWLSDWIQPDVI
KCKKDRSPSSAQQCPLCMNPRTSKGKPLAMVSAAAFQCAKPTIDSSLKSKSLTILEDSSS
AFISPQGFMAPFGSLTLNMTDQSGNEANMVCSIQKPSRTSPIAFTEENDYIVLNTSFSTFL
VCNIDYGHIQPVWQILALYSDSPLILERSHLLSETPQLYYKYKQVAPKPEDIFTNIEADLR
ADPSWLMQDQISLQLNRTATTFSTLQIQYSSDAQITLPRAEMRPVKHKWTMISRDNNTK
LEHTVLVGGTVGLNCPGQGDPTPHVDWLLADGSKVRAPYVSEDGRILIDKSGKLELQM
ADSFDTGVYHCISSNYDDADILTYRITVVEPLVEAYQENGIHHTVFIGETLDLPCHSTGIP
DASISWVIPGNNVLYQSSRDKKVLNNGTLRILQVTPKDQGYYRCVAANPSGVDFLIFQV
SVKMKGQRPLEHDGETEGSGLDESNPIAHLKEPPGAQLRTSALMEAEVGKHTSSTSKRH
NYRELTLQRRGDSTHRRFRENRRHFPPSARRIDPQHWAALLEKAKKNAMPDKRENTTV
SPPPVVTQLPNIPGEEDDSSGMLALHEEFMVPATKALNLPARTVTADSRTISDSPMTNIN
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ATEFQDSDQMGRGREHFQSRPPITVRTMIKDVNVKMLSSTTNKLLLESVNSHQTSVREV
SEPRHNHFYSHTTQILSTSTFPSDPHTAAHSQFPIPRNSTVNIPLFRRFGRQRKIGGRGRIIS
PYRTPVLRRHRYSIFRSTTRGSSEKSTTAFSATVLNVTCLSCLPRELTTATAALSFPSAAPI
TFPKADIARVPSEESTTLVQNPLLLLENKPSVEKTTPTIKYFRTEISQVTPTGAVMTYAPT
SIPMEKTHKVNASYPRVSSTNEAKRDSVITSSLSGAITKPPMTIIAITRFSRRKIPWQQNFV
NNHNPKGRLRNQHKVSLQKSTAVMLPKTSPALPQRQSSPFHFRRLSTSVMQIPSNTLTT
AHHTTTKTHNPGSLPTKKELPFPPLNPMLPSIISKDSSTKSIISTQTAIPATTPTFPASVITYE
TQTERSRAQTIQREQEPQKKNRTDPNISPDQSSGFTTPTAMTPPALAFTHSPPENTTGISST
ISFHSRTLNLTDVIEELAQASTQTLKSTIASETTLSSKSHQSTTTRKASLDTPIPPFLSSSAT
LMPVPISPPFTQRAVTDTRGDSHFRLMTNTVVKLHESSRHNLQMPSSQLEPLTSSTSNLL
HSTPMPALTTVKSQNSKLTPSPWAEQFWHKPYSDIAEKGKKPEVSMLATTGLSEATTLV
SDWDGQKNTKKSDFDKKPVQEATTSKLLPFDSLSRYIFEKPRIVGGKAASFTIPANSDAF
LPCEAVGNPLPTIHWTRVSGLDLSRGNQNSRVQVLPNGTLSIQRVEIQDRFQYLCSASNL
FGTDHLHVTLSVVSYPPRILERRTKEITVHSGSTVELKCRAEGRPSPTVTWILANQTVVSE
SSQGSRQAVVTVDGTLVLHNLSIYDRGFYKCVASNPGGQDSLLVKIQVIAAPPVILEQRR
QVIVGTWGESLKLPCTAKGTPQPSVYWVLSDGTEVKPLQFTNSKLFLFSNGTLYIRNLAS

Date Recue/Date Received 2020-04-01

SDRFTYECIATSSTGSERRVVMLTMEERVTSPRIEAASQKRTEVNFGDKLLLNCSATGEP
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LKPAKIDHKQYFRKQVLHGKDFQVDCKASGSPVPEISWSLPDGTMINNAMQADDSGHR
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SPEVMWIMPDNIFLTAPYYGSRITVHKNGTLEIRNVRLSADFICVARNEGGESVLVVQLE
VLEMLRRPTFRNPRNPFNEKIVAQLGKSTALNCVSVDGNPPPEIIWILPNGTRFSNGPQSY
QYLIASNGSFIISKTTREDAGKYRCAARNKVGYIEKLVILEIGQKPVILTYAPGTVKGISGE
SLSLHCVSDGIPKPNIKWTMPSGYVVDRPQINGKYILHDNGTLVIKEATAYDRGNYICKA
QNSVGHTLITVPVMIVAYPPRITNRPPRSIVTRTGAAFQLHCVALGVPKPEITWEMPDHS
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NO: 16)

Figure 19

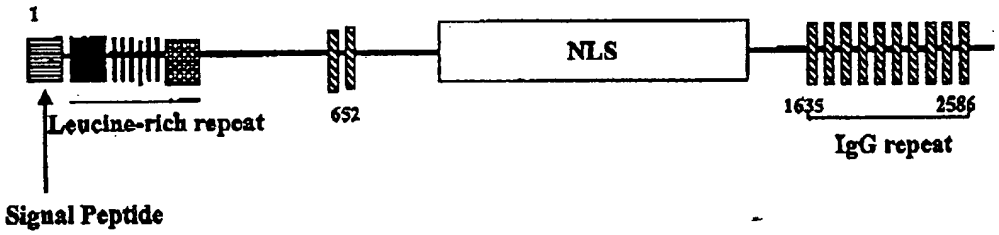
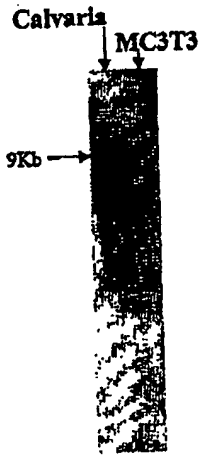


Figure 20

A



B

Cell lines & primary cells		
C6	Rat glioma	-
C2C12	Myoblasts	-
STO	Fibroblasts	-
Bone marrow	Stromal cells	- (+)
PC-3	prostatic carcinoma	-
SAOS-2	osteosarcoma	-
U2OS	osteosarcoma	+
Articular cartilage	chondrocytes	-
ROS	osteosarcoma	-
Calvaria	Osteoblasts	+
C3H10T1/2	mesenchyme	- (+)
MC3T3-E1	preosteoblastic	- (+)

Figure 21

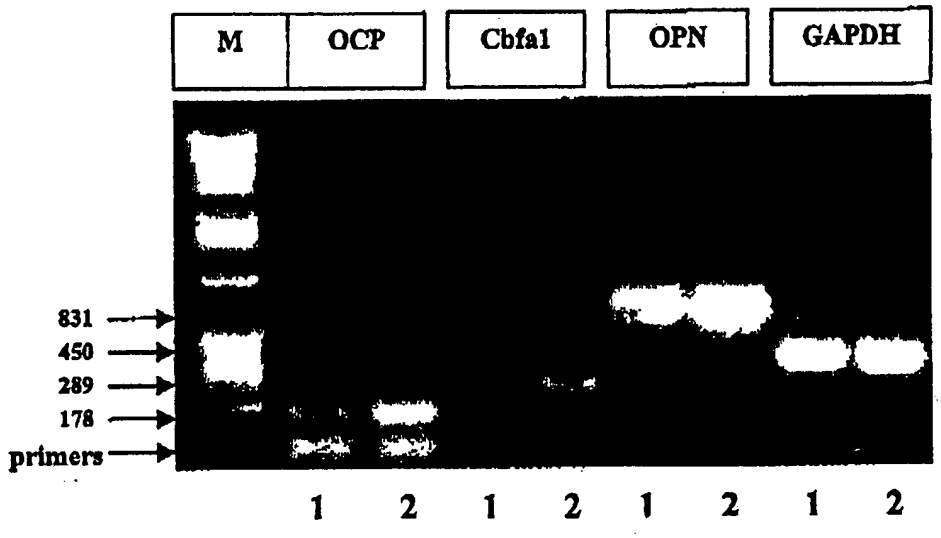


Figure 24

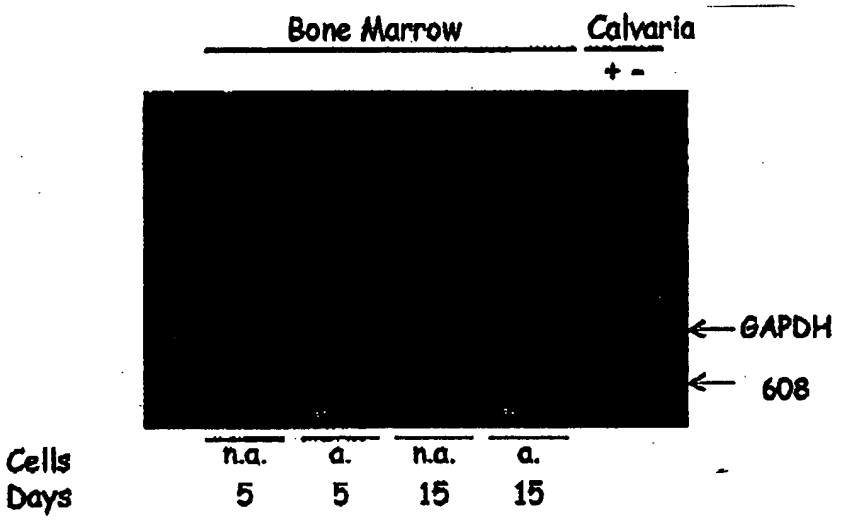


Figure 25

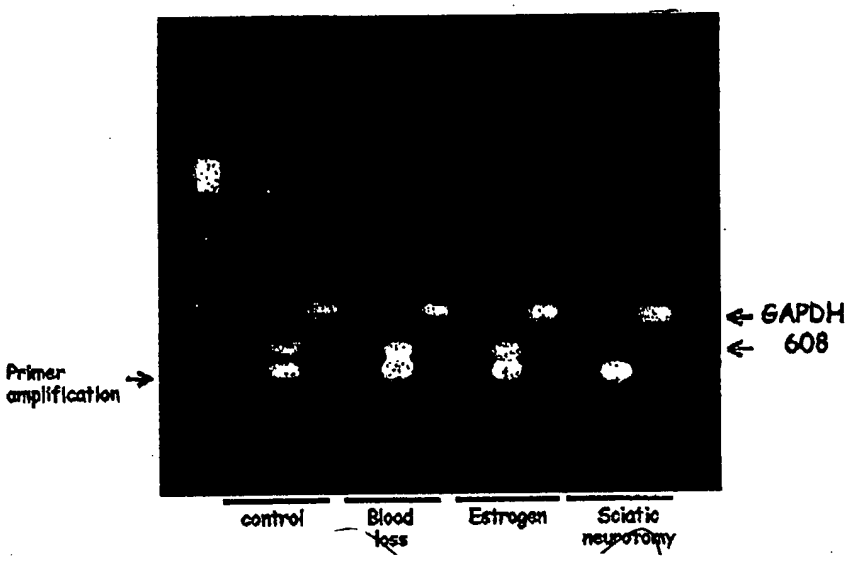


Figure 26

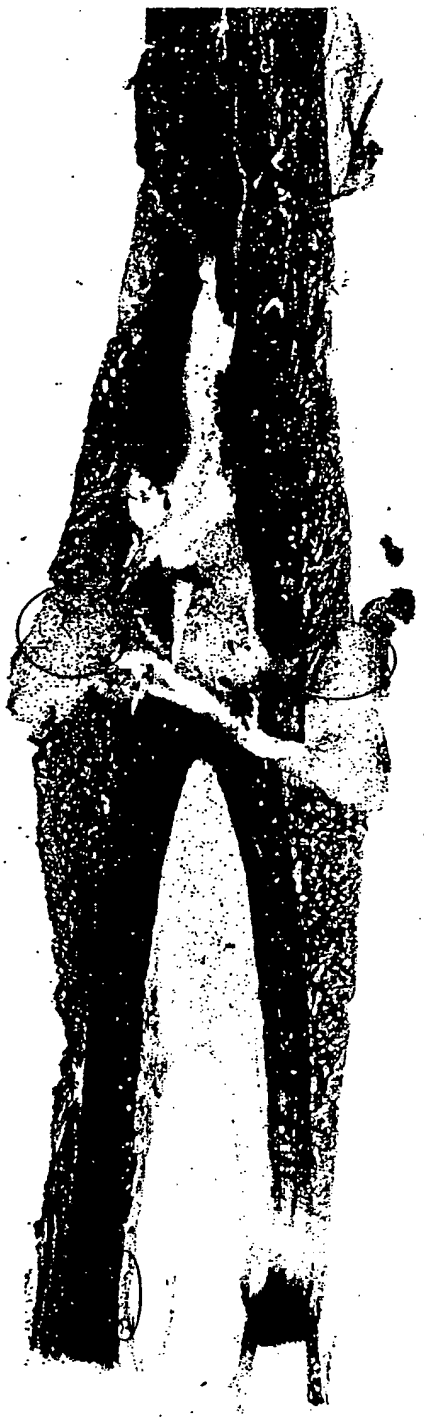


Figure 27

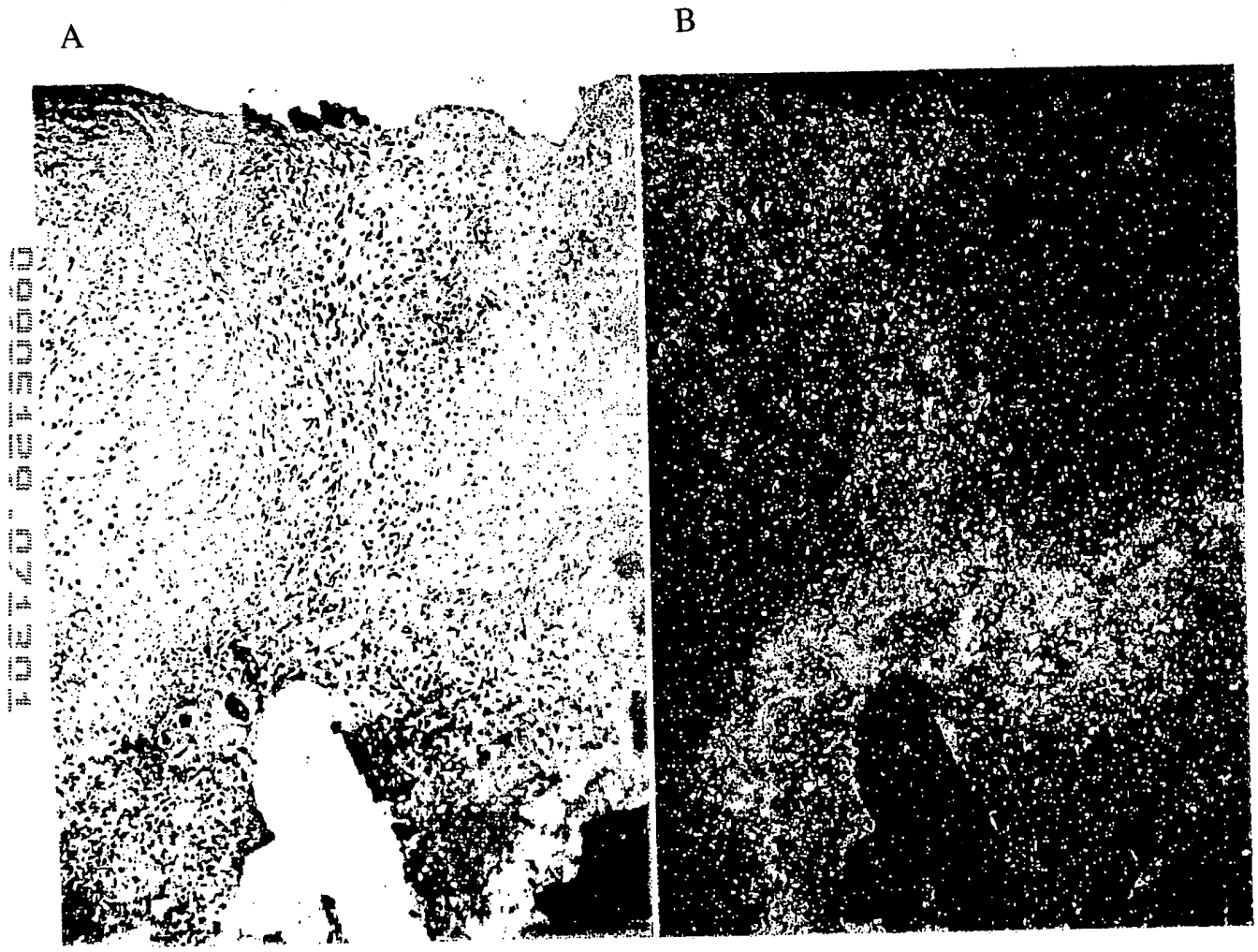


Figure 28

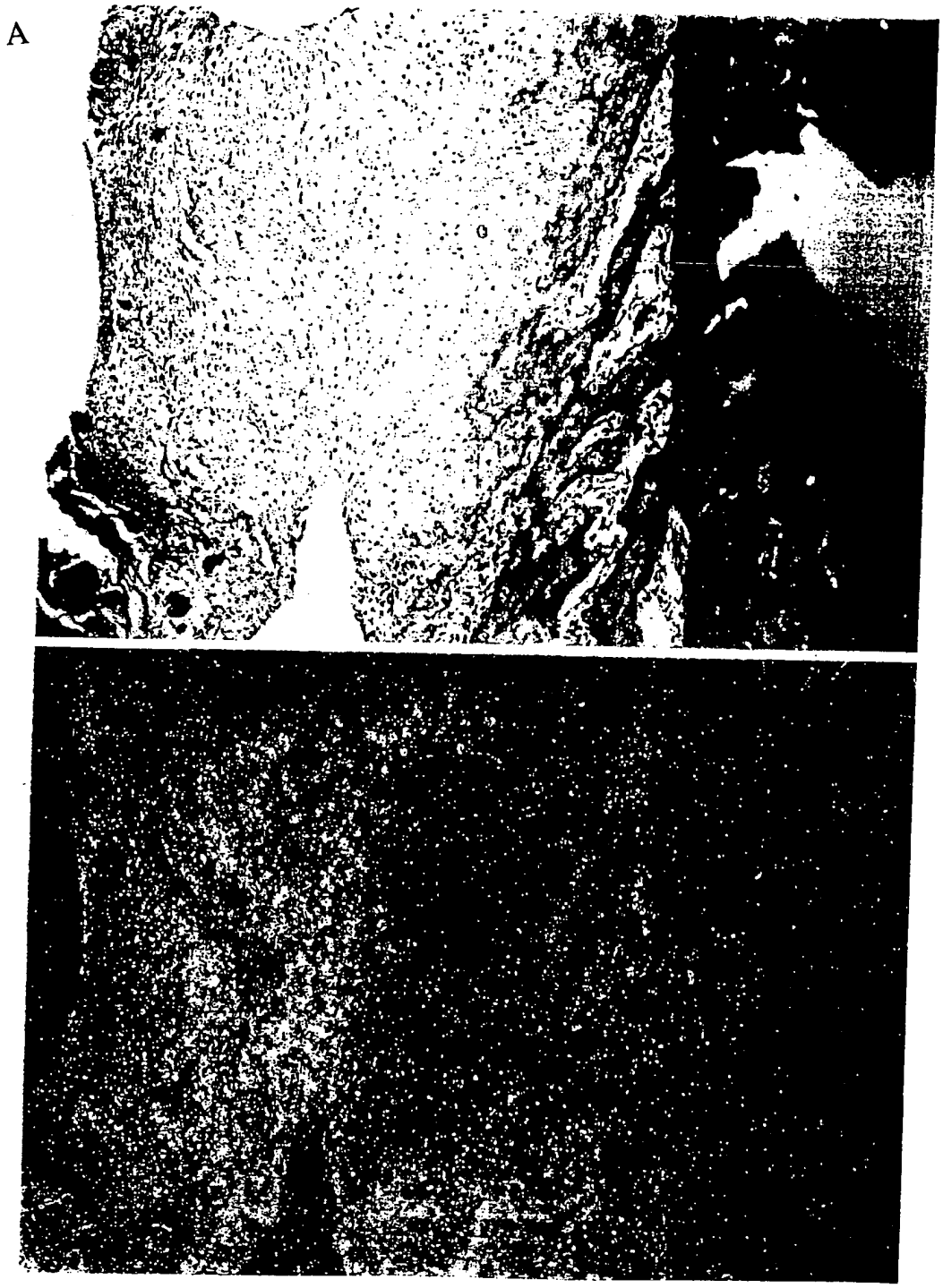


Figure 29

A

B

Figure 30

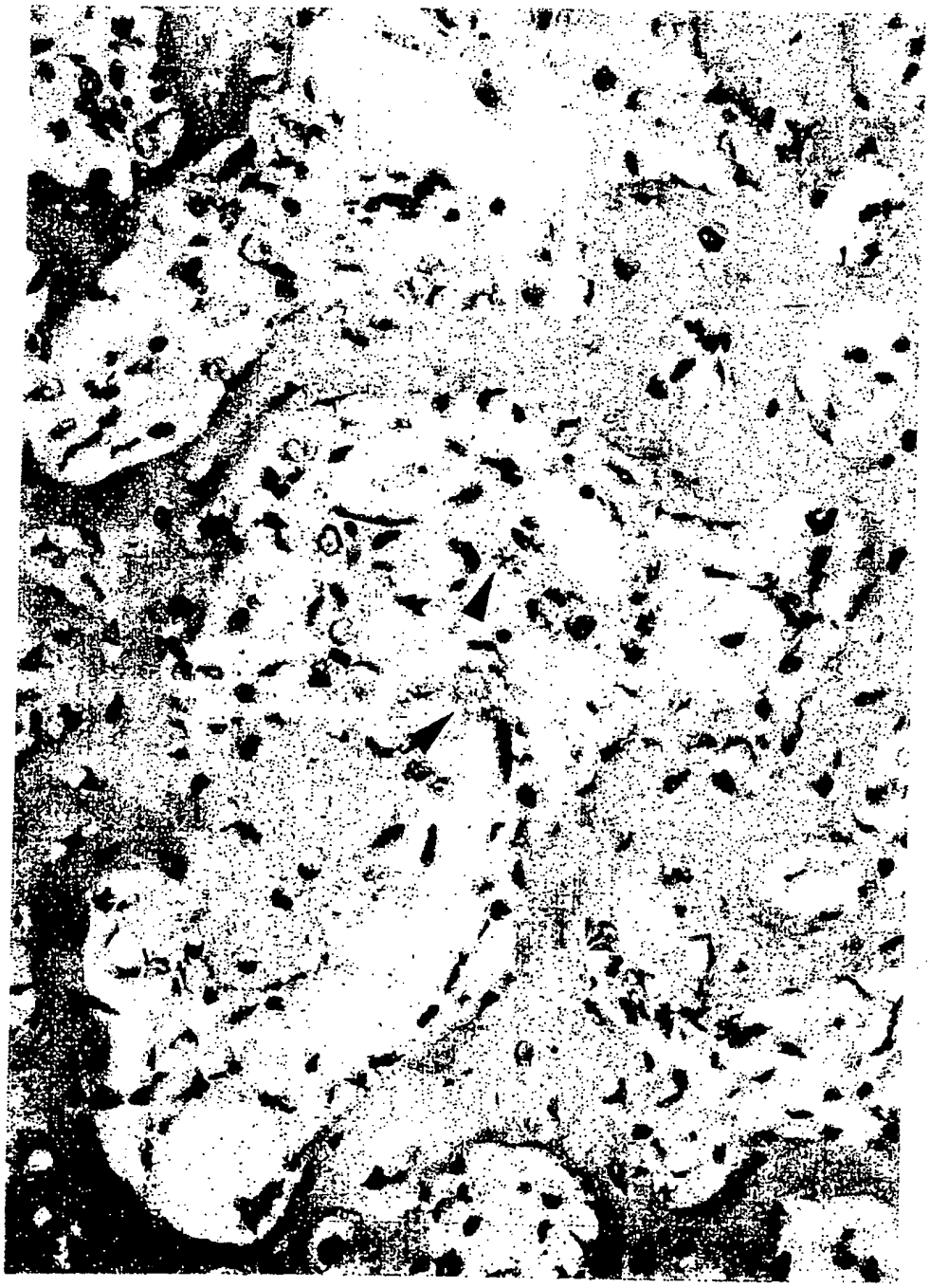


Figure 31

Figure 32

A

B

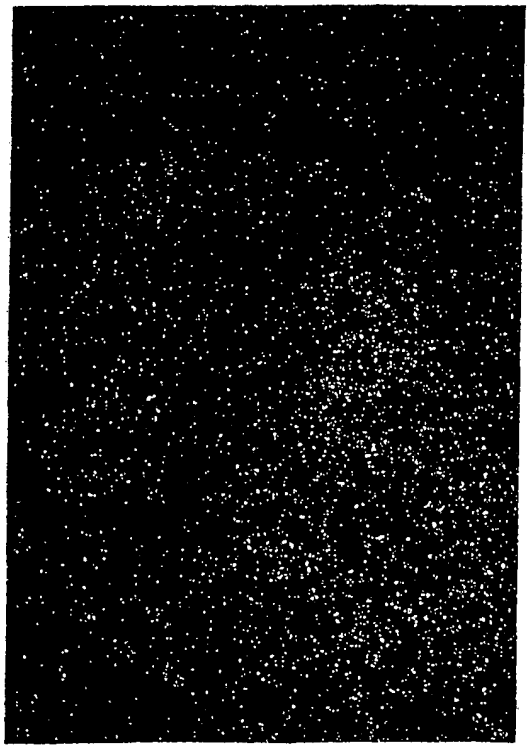


Figure 33

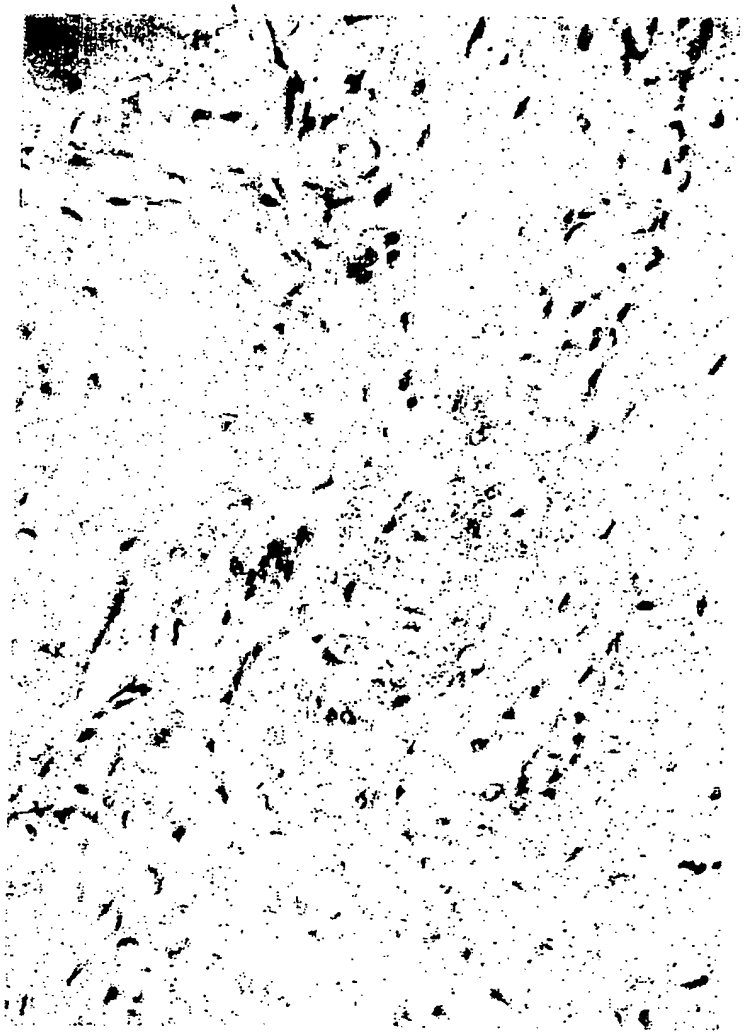


Figure 34

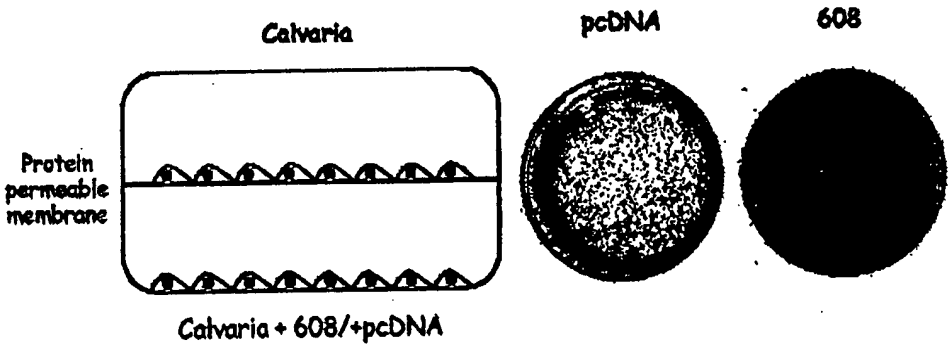


Figure 35

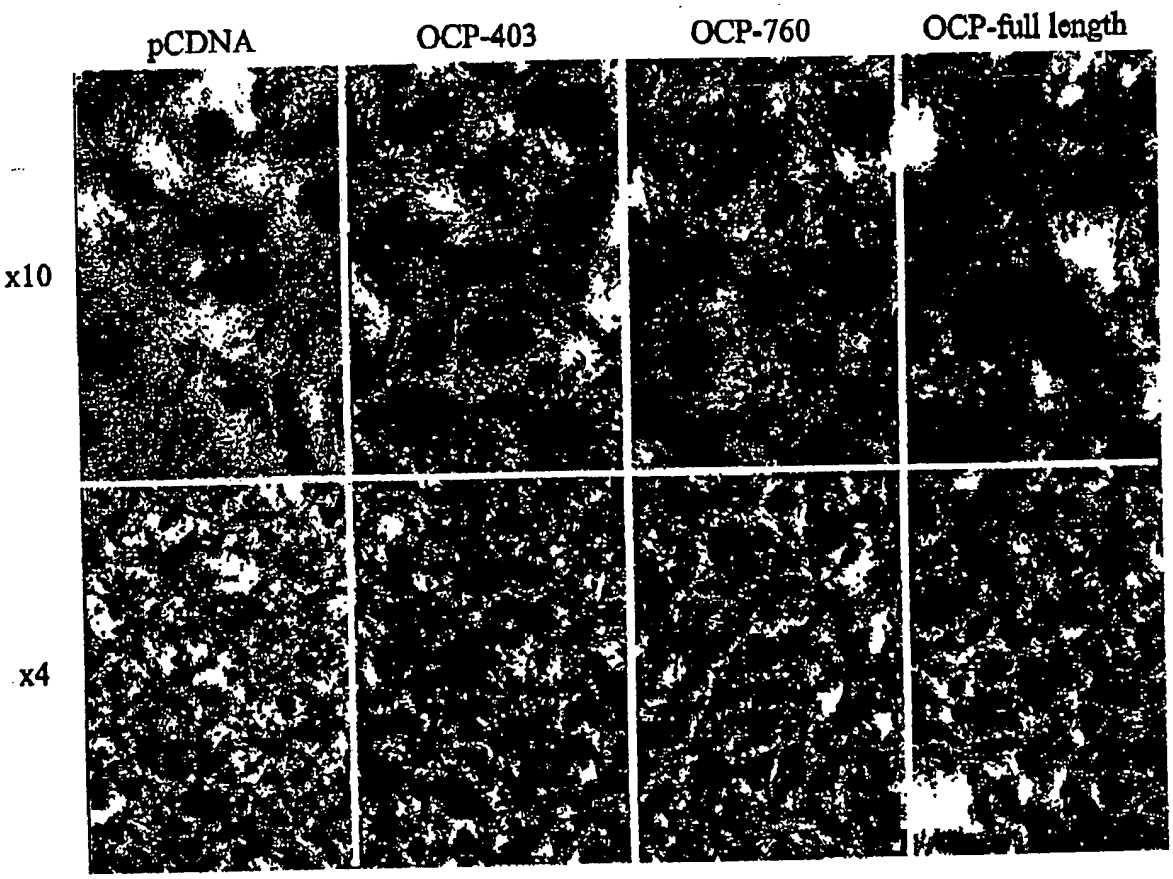


Figure 36

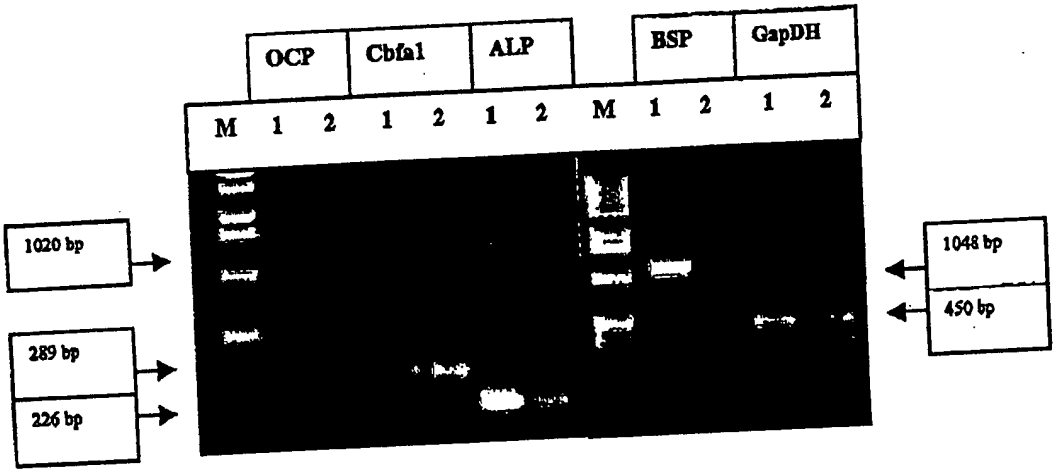


Figure 37

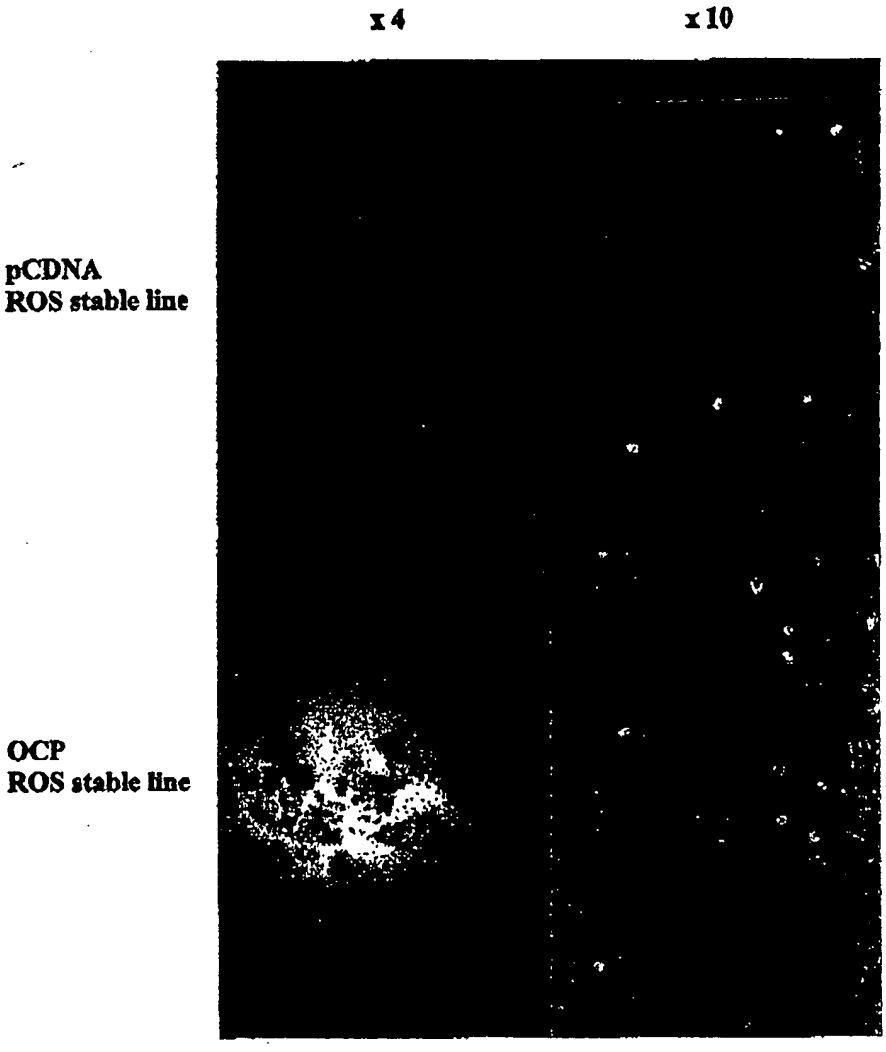


Figure 38

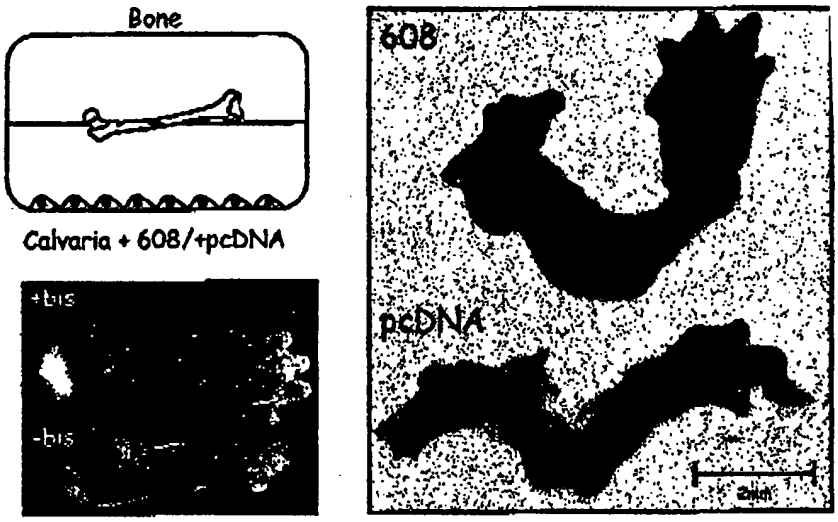


Figure 39

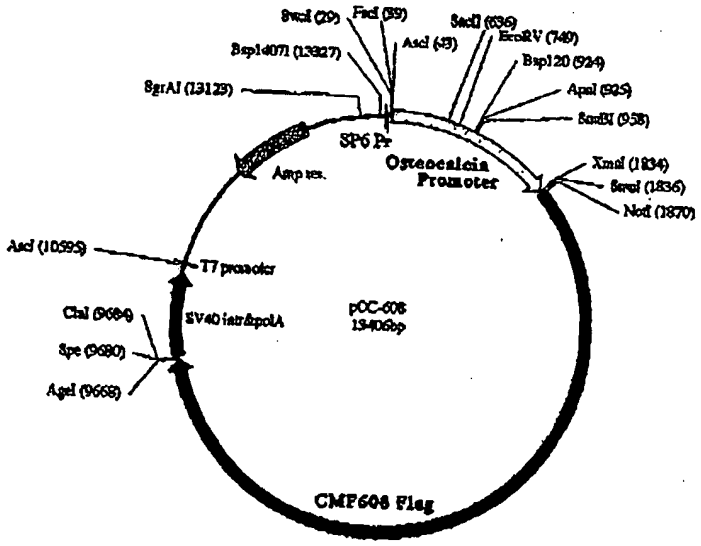


Figure 40

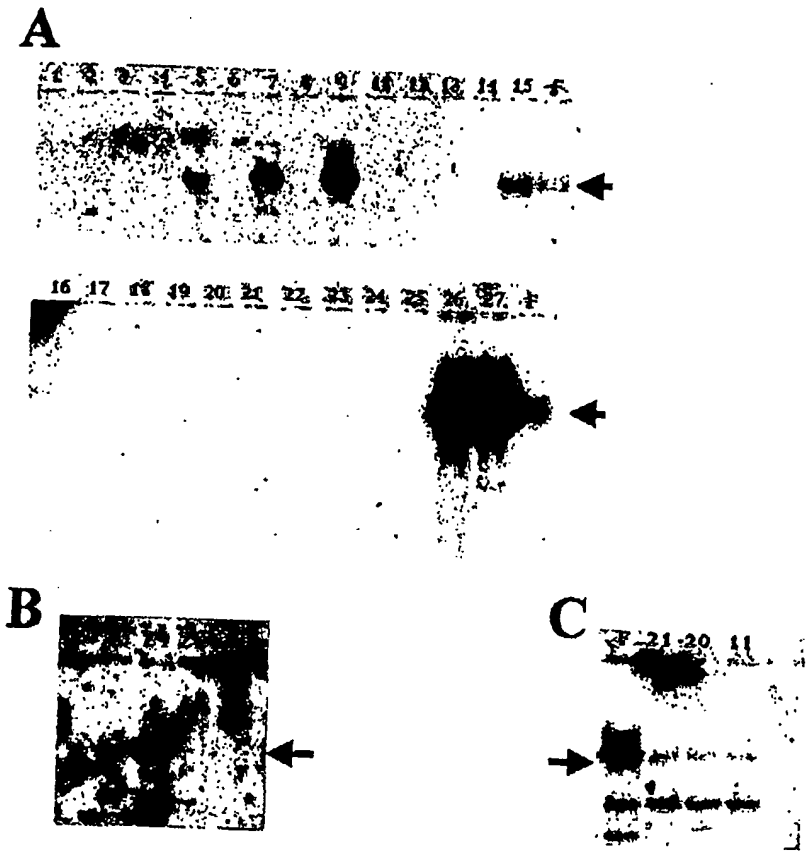
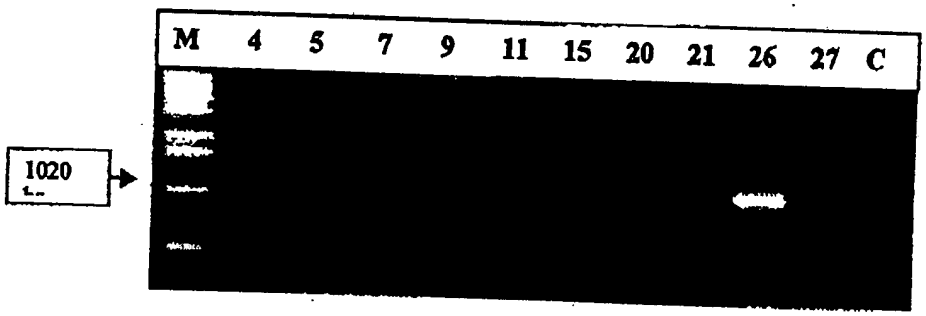


Figure 41

A



B

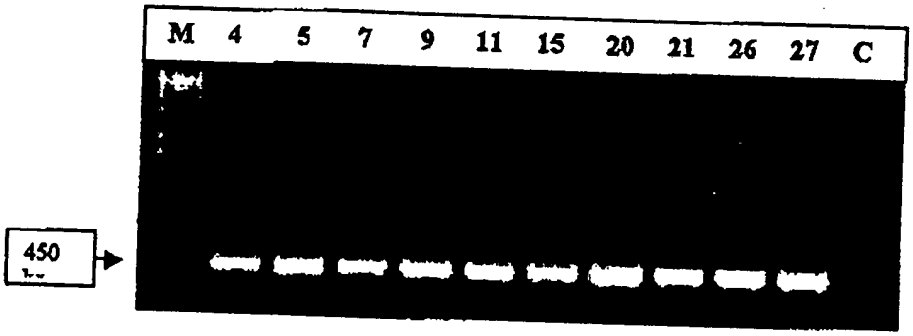
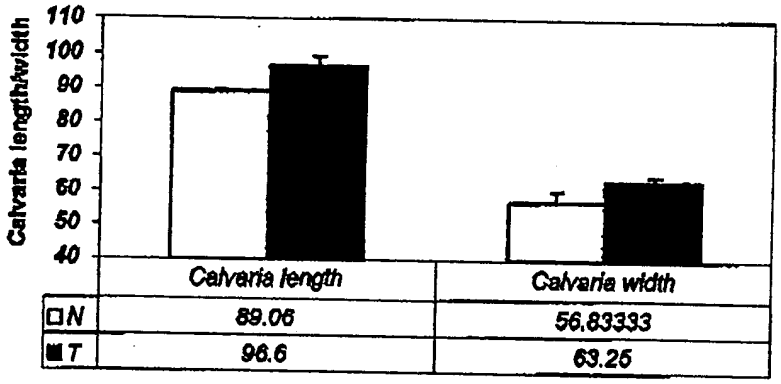


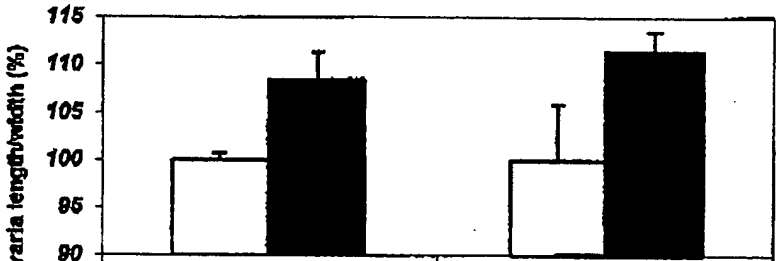
Figure 42

A



	Calvaria length	Calvaria width
N	89.06	56.83333
T	96.6	63.25

B



	Calvaria length	Calvaria width
N	100	100
T	108.5	111.3

Figure 43

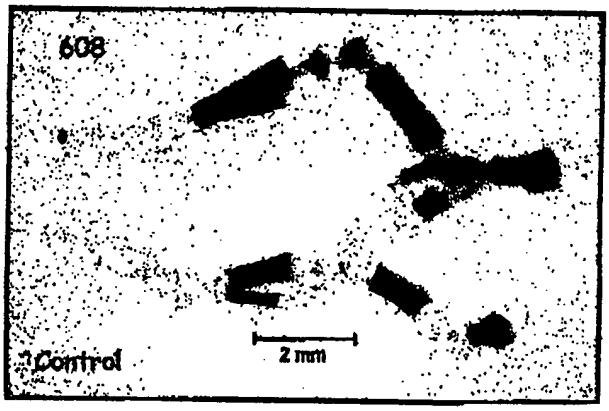


Figure 44

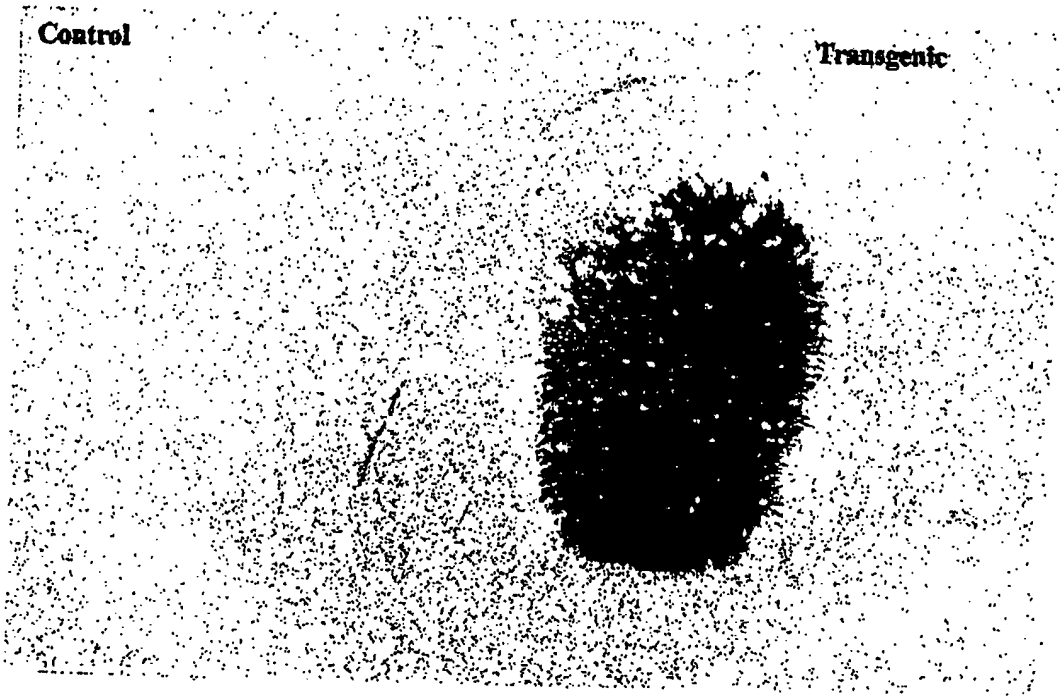
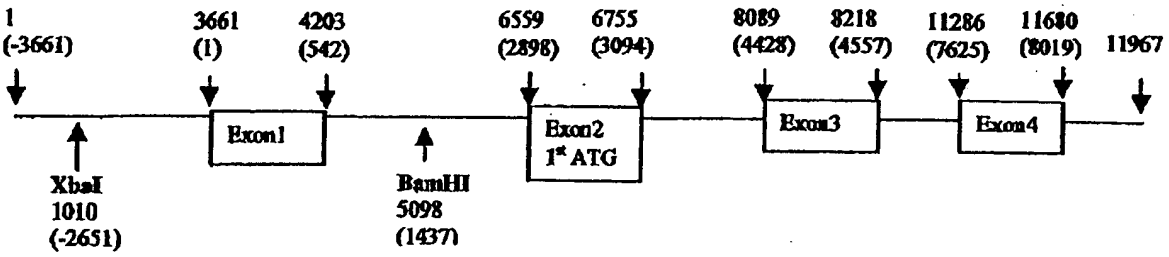


Figure 45



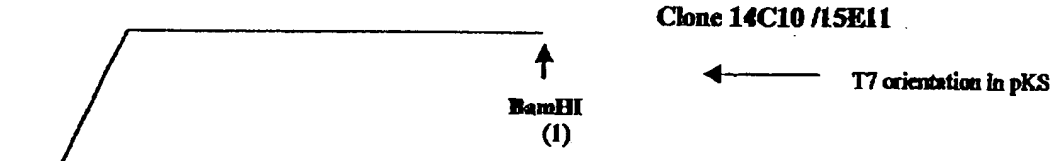


Figure 46

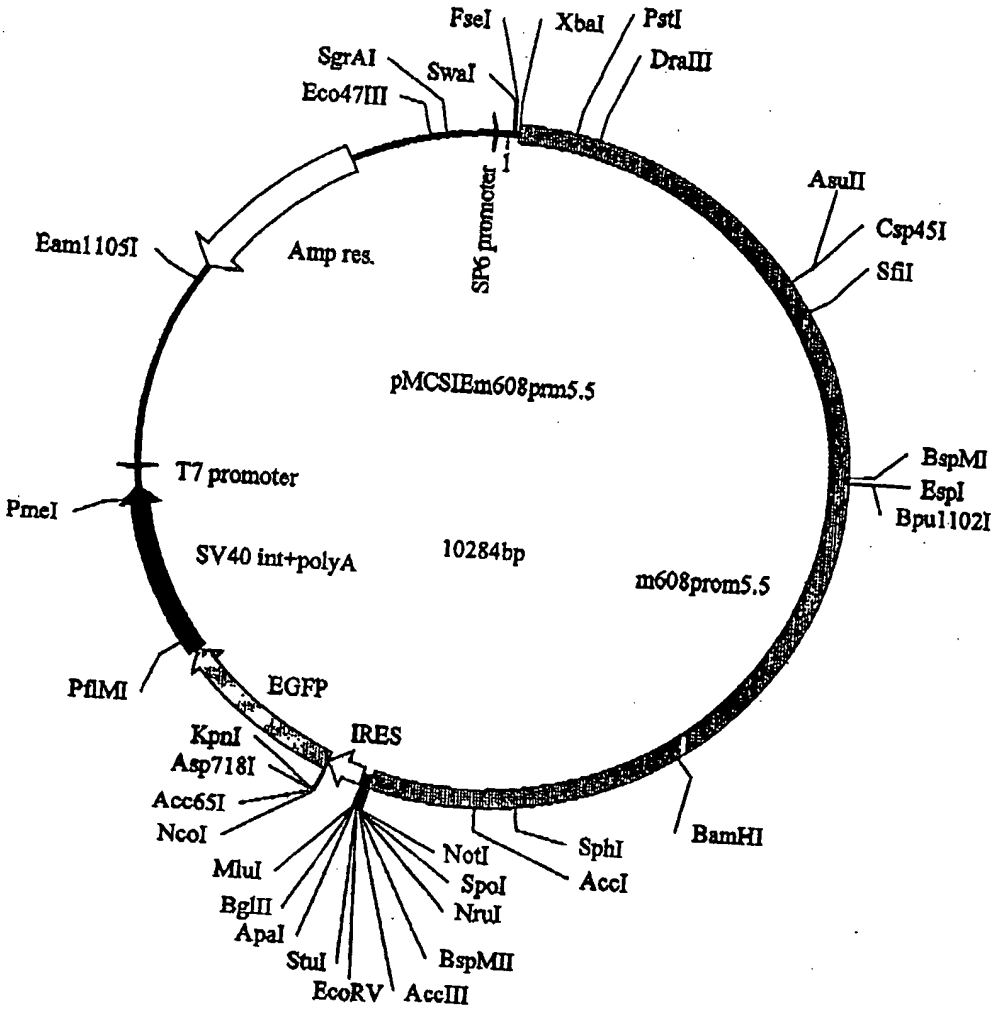


Figure 47

(XbaI)
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(SEQ ID NO:17)

Figure 48

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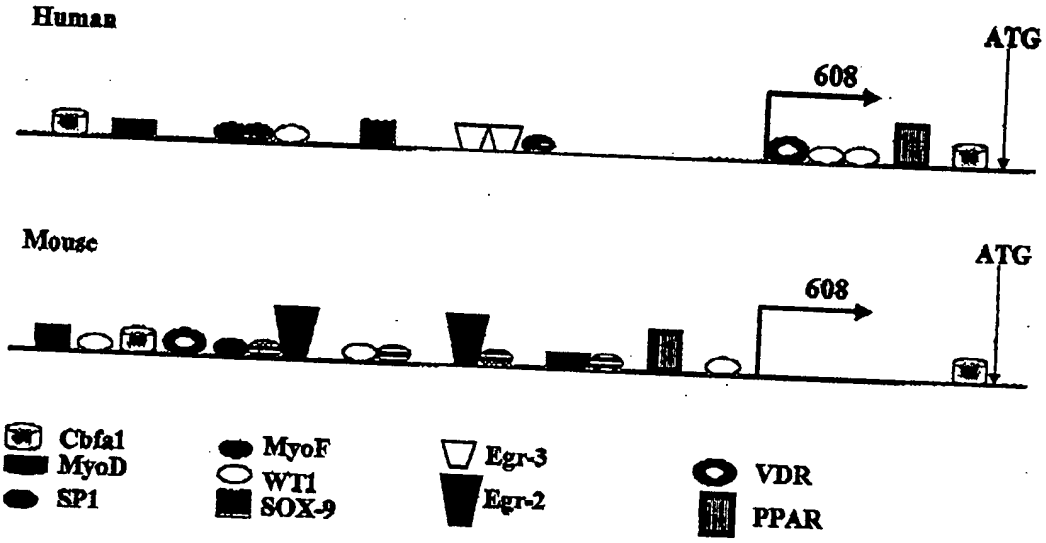
(SEQ ID NO:18)

Figure 49


Human
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608
Mouse
ATG
608
Cbfa1
MyoD
SP1
MyoF
WT1
SOX-9
Egr-3
Egr-2
VDR
PPAR

Figure 50

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12-12-20 02:14:30:00

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Figure 51

MPKRAHWGALSVVLILLWGHPRVALACPHPCACYVPSEVHCTFRSLASVPAGIARHVE
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EEDGGSQLILEKFQLPQWSISLNMTDEHGNMVNLVCDIKKPMDVYKIHLNQTDPPDIDIN
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QRDAGFYKCMAKNILGSDSKTTYIHVF (SEQ ID NO: 21)

Figure 52

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ACGTCTCTGA GGCTACTCCA TTTGGAAGGA AATCTCCTCC ACCAGCTGCA
CCCCAGCACC TTCTCCACGT TCACATTTTT GGATTATTTC AGACTCTCCA
CCATAAGGCA CCTCTACTTA GCAGAGAACA TGGTTAGAAC TCTTCCTGCC
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ACGGCCTGGA CAGGATGGTG GTCTTGCTTT CGGTCACCGT GCAGCAACCT
CAAATCCTAG CCTCCCACTA CCAGGACGTC ACTGTCTACC TGGGAGACAC
CATTGCAATG GAGTGTCTGG CCAAAGGGAC CCCAGCCCCC CAAATTTCCT
GGATCTTCCC TGACAGGAGG GTGTGGCAAA CTGTGTCCCC

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CGTGGAGAGC CGCATCACCC TGCACGAAAA CCGGACCCTT TCCATCAAGG
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GCCGGGGCGG ACAGCCTGGC CATCCGCCTG CACGTGGCGG CACTGCCCCC
CGTTATCCAC CAGGAGAAGC TGGAGAACAT CTCGCTGCCC CCGGGGCTCA
GCATTCACAT TCACTGCACT GCCAAGGCTG CGCCCCTGCC CAGCGTGCGC
TGGGTGCTCG GGGACGGTAC CCAGATCCGC CCCTCGCAGT TCCTCCACGG
GAACTTGTTT GTTTTCCCCA ACGGGACGCT CTACATCCGC AACCTCGCGC
CCAAGGACAG CGGGCGCTAT GAGTGCGTGG CCGCCAACCT GGTAGGCTCC
GCGCGCAGGA CGGTGCAGCT GAACGTGCAG CGTGCAGCAG CCAACGCGCG
CATCACGGGC ACCTCCCCGC GGAGGACGGA CGTCAGGTAC GGAGGAACCC
TCAAGCTGGA CTGCAGCGCC TCGGGGGACC CCTGGCCGCG CATCCTCTGG
AGGCTGCCGT CCAAGAGGAT GATCGACGCG CTCTTCAGTT TTGATAGCAG
AATCAAGGTG TTTGCCAATG GGACCCTGGT GGTGAAATCA GTGACGGACA
AAGATGCCGG AGATTACCTG TGCGTAGCTC GAAATAAGGT TGGTGATGAC
TACGTGGTGC TCAAAGTGGA TGTGGTGATG AAACCGGCCA AGATTGAACA
CAAGGAGGAG AACGACCACA AAGTCTTCTA CGGGGGTGAC CTGAAAGTGG
ACTGTGTGGC CACCGGGCTT CCCAATCCCG AGATCTCCTG GAGCCTCCCA
GACGGGAGTC TGGTGAACTC CTTCATGCAG TCGGATGACA GCGGTGGACG
CACCAAGCGC TATGTCGTCT TCAACAATGG GACACTCTAC TTTAACGAAG
TGGGGATGAG GGAGGAAGGA GACTACACCT GCTTTGCTGA AAATCAGGTC
GGGAAGGACG AGATGAGAGT CAGAGTCAAG GTGGTGACAG CGCCCGCCAC
CATCCGGAAC AAGACTTACT TGGCGGTTCA GGTGCCCTAT GGAGACGTGG
TCACTGTAGC CTGTGAGGCC AAAGGAGAAC CCATGCCCAA GGTGACTTGG
TTGTCCCCAA CCAACAAGGT GATCCCCACC TCCTCTGAGA AGTATCAGAT
ATACCAAGAT GGCACTCTCC TTATTCAGAA AGCCCAGCGT TCTGACAGCG
GCAACTACAC CTGCCTGGTC AGGAACAGCG CGGGAGAGGA TAGGAAGACG
GTGTGGATTC ACGTCAACGT CCAGCCACCC AAGATCAACG GTAACCCCAA
CCCCATCACC ACCGTGCGGG AGATAGCAGC CGGGGGCAGT CGGAAACTGA
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CCCGAGGGTG TGGTTCTGCC AGCTCCATAC TATGGAAACC GGATCACTGT
CCATGGCAAC GGTTCCCTGG ACATCAGGAG TTTGAGGAAG AGCGACTCCG
TCCAGCTGGT ATGCATGGCA CGCAACGAGG GAGGGGAGGC GAGGTTGATC
GTGCAGCTCA CTGTCCTGGA GCCCATGGAG AAACCCATCT TCCACGACCC
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GCTCTGCCGC GGGGACCCCG ACACCCAGCC TGGTGTGGGT CCTTCCCAAT
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ACCGCTGCGT GGCCCGCAAT GCCGCTGGCC ACACGGAGAG GCTGGTCTCC
CTGAAGGTGG GACTGAAGCC AGAAGCAAAC AAGCAGTATC ATAACCTGGT
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CGGGAACACC GTGAAACTGA ACTGCATGGC TATGGGGATT CCCAAAGCTG
ACATCACGTG GGAGTTACCG GATAAGTCGC ATCTGAAGGC AGGGGTTCAG
GCTCGTCTGT ATGGAAACAG ATTTCTTCAC CCCCAGGGAT CACTGACCAT
CCAGCATGCC ACACAGAGAG ATGCCGGCTT CTACAAGTGC ATGGCAAAAA
ACATTCTCGG CAGTGACTCC AAAACAACTT ACATCCACGT CTTCTGAAAT
GTGGATTCCA GAATGATTGC TTAGGAACTG ACAACAAAGC GGGGTTTGTA
AGGGAAGCCA GGTTGGGGAA TAGGAGCTCT TAAATAATGT GTCACAGTGC
ATGGTGGCCT CTGGTGGGTT TCAAGTTGAG GTTGATCTTG ATCTACAATT
GTTGGGAAAA GGAAGCAATG CAGACACGAG AAGGAGGGCT CAGCCTTGCT
GAGACACTTT CTTTTGTGTT TACATCATGC CAGGGGCTTC ATTCAGGGTG
TCTGTGCTCT GACTGCAATT TTTCTTCTTT TGCAAATGCC ACTCGACTGC
CTTCATAAGC GTCCATAGGA TATCTGAGGA ACATTCATCA AAAATAAGCC
ATAGACATGA ACAACACCTC ACTACCCCAT TGAAGACGCA TCACCTAGTT
AACCTGCTGC AGTTTTTACA TGATAGACTT TGTTCCAGAT TGACAAGTCA
TCTTTCAGTT ATTTCCTCTG TCACTTCAAA ACTCCAGCTT GCCCAATAAG
GATTTAGAAC CAGAGTGACT GATATATATA TATATATTTT AATTCAGAGT
TACATACATA CAGCTACCAT TTTATATGAA AAAAGAAAAA CATTTCTTCC
TGGAACTCAC TTTTTATATA ATGTTTTATA TATATATTTT TTCCTTTCAA
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ATAAATTATT GGTCTTTACA AGACTTGGAT ACATTACAGC AGACATGGAA
ATATAATTTT AAAAAATTTC TCTCCAACCT CCTTCAAATT CAGTCACCAC
TGTTATATTA CCTTCTCCAG GAACCCTCCA GTGGGGAAGG CTGCGATATT
AGATTTCCTT GTATGCAAAG TTTTTGTTGA AAGCTGTGCT CAGAGGAGGT
GAGAGGAGAG GAAGGAGAAA ACTGCATCAT AACTTTACAG AATTGAATCT
AGAGTCTTCC CCGAAAAGCC CAGAAACTTC TCTGCAGTAT CTGGCTTGTC
CATCTGGTCT AAGGTGGCTG CTTCTTCCCC AGCCATGAGT CAGTTTGTGC
CCATGAATAA TACACGACCT GTTATTTCCA TGACTGCTTT ACTGTATTTT
TAAGGTCAAT ATACTGTACA TTTGATAATA AAATAATATT CTCCCAAAAA AAAAA

Figure 5

Human OCP: nucleotide sequence of ORF

ATGAAGGTAAAAGGCAGAGGAATCACCTGCTTGCTGGTCTCCTTTGCTGTGATCTGC
CTGGTCGCCACCCCTGGGGGCAAGGCCTGTCCTCGCCGCTGTGCCTGTTATATGCCT
ACGGAGGTACACTGCACATTTCGGTACCTGACTTCCATCCCAGACAGCATCCCGCCC
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Replacement Sheet

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TCTGGGATATACAAATGCACAGCAAAGAACCCACTTGGTAGTGATTATGCAGCAACG
TATATTCAAGTAATCTGA

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Figure 5B

Human OCP: predicted amino acid sequence

MKVKGRGITC LLVSFAVICL VATPGGKACP RRCACYMPTE VHCTFRYLTS
IPDSIPPNVE RINLGYNSLV RLMETDFSGL TKLELLMLHS NGIHTIPDKT
FSDLQALQVL KMSYNKVRKL QKDTFYGLRS LTRLHMDHNN IEFINPEVFY
GLNFLRLVHL EGNQLTKLHP DTFVSLSYLQ IFKISFIKFL YLSDNFLTSL
PQEMVSYMPD LDSLYLHGNP WTCDCHLKWL SDWIQEKPDV IKCKKDRSPS
SAQQCPLCMN PRTSKGKPLA MVSAAAFQCA KPTIDSSLKS KSLTILEDSS
SAFISPQGFM APFGSLTLNM TDQSGNEANM VCSIQKPSRT SPIAFTEEND
YIVLNTSFST FLVCNIDYGH IQPVWQILAL YSDSPLILER SHLLSETPQL
YYKYKQVAPK PEDIFTNIEA DLRADPSWLM QDQISLQLNR TATTFSTLQI
QYSSDAQITL PRAEMRPVKH KWTMISRDNN TKLEHTVLVG GTVGLNCPGQ
GDPTPHVDWL LADGSKVRAP YVSEDGRILI DKSGKLELQM ADSFDTGVYH
CISSNYDDAD ILTYRITVVE PLVEAYQENG IHHTVFIGET LDLPCHSTGI
PDASISWVIP GNNVLYQSSR DKKVLNNGTL RILQVTPKDQ GYYRCVAANP
SGVDFLIFQV SVKMKGQRPL EHDGETEGSG LDESNPIAHL KEPPGAQLRT
SALMEAEVGK HTSSTSKRHN YRELTLQRRG DSTHRRFREN RRHFPPSARR
IDPQHWAALL EKAKKNAMPD KRENTTVSPP PVVTQLPNIP GEEDDSSGML
ALHEEFMVPA TKALNLPART VTADSRTISD SPMTNINYGT EFSPVVNSQI
LPPEEPTDFK LSTAIKTTAM SKNINPTMSS QIQGTTNQHS STVFPLLLGA
TEFQDSDQMG RGREHFQSRP PITVRTMIKD VNVKMLSSTT NKLLLESVNT
TNSHQTSVRE VSEPRHNHFY SHTTQILSTS TFPSDPHTAA HSQFPIPRNS
TVNIPLFRRF GRQRKIGGRG RIISPYRTPV LRRHRYSIFR STTRGSSEKS
TTAFSATVLN VTCLSCLPRE RLTTATAALS FPSAAPITFP KADIARVPSE
ESTTLVQNPL LLLENKPSVE KTTPTIKYFR TEISQVTPTG AVMTYAPTSI
PMEKTHKVNA SYPRVSSTNE AKRDSVITSS LSGAITKPPM TIIAITRFSR
RKIPWQQNFV NNHNPKGRLR NQHKVSLQKS TAVMLPKTSP ALPQRQSSPF
HFTTLSTSVM QIPSNTLTTA HHTTTKTHNP GSLPTKKELP FPPLNPMLPS
IISKDSSTKS IISTQTAIPA TTPTFPASVI TYETQTERSR AQTIQREQEP
QKKNRTDPNI SPDQSSGFTT PTAMTPPALA FTHSPPENTT GISSTISFHS
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PFLSSSATLM PVPISPPFTQ RAVTDTRGDS HFRLMTNTVV KLHESSRHNL
QMPSSQLEPL TSSTSNLLHS TPMPALTTVK SQNSKLTPSP WAEYQFWHKP
YSDIAEKGKK PEVSMLATTG LSEATTLVSD WDGQKNTKKS DFDKKPVQEA
TTSKLLPFDS LSRYIFEKPR IVGGKAASFT IPANSDAFLP CEAVGNPLPT
IHWTRVSGLD LSRGNQNSRV QVLPNGTLSI QRVEIQDRGQ YLCSASNLFG
TDHLHVTLSV VSYPPRILER RTKEITVHSG STVELKCRAE GRPSPTVTWI
LANQTVVSES SQGSRQAVVT VDGTLVLHNL SIYDRGFYKC VASNPGGQDS
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MLTMEERVTS PRIEAASQKR TEVNFGDKLL LNCSATGEPK PQIMWRLPSK
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LKPAKIDHKQ YFRKQVLHGK DFQVDCKASG SPVPEISWSL PDGTMINNAM
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FSIDRYTFHA NGSLTINKVK LLDSGEYVCV ARNPSGDDTK MYKLDVVSKP
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RRPTFRNPFN EKIVAQLGKS TALNCSVDGN PPPEIIWILP NGTRFSNGPQ
SYQYLIASNG SFIISKTTRE DAGKYRCAAR NKVGYIEKLV ILEIGQKPVI

LTYAPGTVKG ISGESLSLHC VSDGIPKPNI KWTMPSGYVV DRPQINGKYI
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PRSIVTRTGA AFQLHCVALG VPKPEITWEM PDHSLLSTAS KERTHGSEQL
HLQGTLVIQN PQTSDSGIYK CTAKNPLGSD YAATYIQVI*